

SEQUENCE LISTING

(1) GENERAL INFORMATION:



(i) APPLICANT: Jacobs, Kenneth
 McCoy, John M.
 LaVallie, Edward R.
 Racie, Lisa A.
 Treacy, Maurice
 Spaulding, Vikki
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 Howes, Steven H.
 Fechtel, Kim

(ii) TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
 ENCODING THEM

(iii) NUMBER OF SEQUENCES: 231

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.
 (B) STREET: 87 CambridgePark Drive
 (C) CITY: Cambridge
 (D) STATE: MA
 (E) COUNTRY: U.S.A.
 (F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/746,783
 (B) FILING DATE: 2000-DEC-21
 (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Milasincic, Debra J.
 (B) REGISTRATION NUMBER: 46,931

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2043 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGAATGCCC CATGCGCACC CCACAGCTCG CGCTCCTGCA AGTGTTCTTT CTGGTGTTC

CCGATGGCGT CCGGCCTCAG CCCTCTTCCT CCCCATCAGG GGCAGTGCCC ACGTCTTTGG	120
AGCTGCAGCG AGGGACGGAT GGCGBAACCC TCCAGTCCCC TTCAGAGGCG ACTGCAACTC	180
GGCCGGCCGT GCCTGGACTC CCTACAGTGG TCCCTACTCT CGTGA CTCCC TCGGCCCTG	240
GGAATAGGAC TGTGGACCTC TTCCCAGTCT TACCGATCTG TGTCTGTGAC TTGACTCCTG	300
GAGCCTGCGA TATAAATTGC TGCTGCGACA GGGACTGCTA TCTTCTCCAT CCGAGGACAG	360
TTTTCTCCTT CTGCCTTCCA GGCAGCGTAA GGTCTTCAAG CTGGGTTTGT GTAGACAACT	420
CTGTTATCTT CAGGAGTAAT TCCCCGTTTC CTTCAAGAGT TTTCATGGAT TCTAATGGAA	480
TCAGGCAGTT TTGTGTCCAT GTGAACAACT CAAACTTAAA CTATTTCCAG AAGCTTCAAA	540
AGGTCAATGC AACCAACTTC CAGGCCCTGG TTGCAGAGTT TGGAGGCGAA TCATTCACTT	600
CAACATTCCA AACTCAATCA CCACCATCTT TTTACAGGGC CGGGGACCCC ATTCTTACTT	660
ACTTCCCCAA GTGGTCTGTA ATAAGCTTGC TGAGACAACC TGCAGGAGTT GGAGCTGGGG	720
GACTCTGTGC TGAAAGCAAT CCTGCAGGTT TCCTAGAGAG TAAAAGTACA ACTTGCACTC	780
GTTTTTTTCA AGAACCTGGC TAGTAGCTGT ACCTTGATT CAGCCCTCAA TGCTGCCTCT	840
TACTATAACT TCACAGTCTT AAAGGTTCCA AGAAGCATGA CTGATCCACA GAATATGGAG	900
TTCCAGGTTT CTGTAATACT TACCTCACAG GCTAATGCTC CTCTGTTGGC TGGAAACACT	960
TGTCAGAATG TAGTTTCTCA GGTCACCTAT GAGATAGAGA CCAATGGGAC TTTTGAATC	1020
CAGAAAGTTT CTGTCAGTTT GGGACAAACC AACCTGACTG TTGAGCCAGG CGCTTCCTTA	1080
CAGCAACACT TCATCCTTCG CTTCAGGGCT TTTCAACAGA GCACAGCTGC TTCTCTCACC	1140
AGTCCTAGAA GTGGGAATCC TGGCTATATA GTTGGGAAGC CACTCTTGGC TCTGACTGAT	1200
GATATAAGTT ACTCAATGAC CCTCTTACAG AGCCAGGGTA ATGGAAGTTG CTCTGTTAAA	1260
AGACATGAAG TGCAGTTTGG AGTGAATGCA ATATCTGGAT GCAAGCTCAG GTTGAAGAAG	1320
GCAGACTGCA GCCACTTGCA GCAGGAGATT TATCAGACTC TTCATGGAAG GCCCAGACCA	1380
GAGTATGTTG CCATCTTTGG TAATGCTGAC CCAGCCCAGA AAGGAGGGTG GACCAGGATC	1440
CTCAACAGGC ACTGCAGCAT TTCAGCTATA AACTGTACTT CCTGCTGTCT CATACCAGTT	1500
TCCCTGGAGA TCCAGGTATT GTGGGCATAT GTAGGTCTCC TGTCCAACCC GCAAGCTCAT	1560
GTATCAGGAG TTCGATTCTT ATACCAGTGC CAGTCTATAC AGGATTCTCA GCAAGTTACA	1620
GAAGTATCTT TGACAACTCT TGTGAACTTT GTGGACATTA CCCAGAAGCC ACAGCCTCCA	1680
AGGGGCCAAC CCAAATGGA CTGGAAATGG CCATTCGACT TCTTTCCCTT CAAAGTGGCA	1740
TTCAGCAGAG GAGTATTCTC TCAAAAATGC TCAGTCTCTC CCATCCTTAT CCTGTGCCTC	1800
TTAGAACTTG GAGTTCTCAA CCTAGAGACT ATGTGAAGAA AAGAAAATAA TCAGATTTC	1860
GTTTTCCCTA TGAGAACTC TGAGGCAGCC ACTTATCTTG GCTAAATAGA ACCTCACCTG	1920

CTCATGACCA GAGAGCATTT AGGATAATAG AGGACCTAAC TGAAGGAATC CTTGTATATG 1980
 AAAGGAGTTA TTTTAGAAAA GCAATAAAAA TATTTTATTC ATCATAAAAA AAAAAAAAAA 2040
 AAA 2043

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Thr Pro Gln Leu Ala Leu Leu Gln Val Phe Phe Leu Val Phe
 1 5 10 15
 Pro Asp Gly Val Arg Pro Gln Pro Ser Ser Ser Pro Ser Gly Ala Val
 20 25 30
 Pro Thr Ser Leu Glu Leu Gln Arg Gly Thr Asp Gly Gly Thr Leu Gln
 35 40 45
 Ser Pro Ser Glu Ala Thr Ala Thr Arg Pro Ala Val Pro Gly Leu Pro
 50 55 60
 Thr Val Val Pro Thr Leu Val Thr Pro Ser Ala Pro Gly Asn Arg Thr
 65 70 75 80
 Val Asp Leu Phe Pro Val Leu Pro Ile Cys Val Cys Asp Leu Thr Pro
 85 90 95
 Gly Ala Cys Asp Ile Asn Cys Cys Cys Asp Arg Asp Cys Tyr Leu Leu
 100 105 110
 His Pro Arg Thr Val Phe Ser Phe Cys Leu Pro Gly Ser Val Arg Ser
 115 120 125
 Ser Ser Trp Val Cys Val Asp Asn Ser Val Ile Phe Arg Ser Asn Ser
 130 135 140
 Pro Phe Pro Ser Arg Val Phe Met Asp Ser Asn Gly Ile Arg Gln Phe
 145 150 155 160
 Cys Val His Val Asn Asn Ser Asn Leu Asn Tyr Phe Gln Lys Leu Gln
 165 170 175
 Lys Val Asn Ala Thr Asn Phe Gln Ala Leu Val Ala Glu Phe Gly Gly
 180 185 190
 Glu Ser Phe Thr Ser Thr Phe Gln Thr Gln Ser Pro Pro Ser Phe Tyr
 195 200 205
 Arg Ala Gly Asp Pro Ile Leu Thr Tyr Phe Pro Lys Trp Ser Val Ile
 210 215 220

ATTY DOCKET NO.: GIN-6054CP

Ser Leu Leu Arg Gln Pro Ala Gly Val Gly Ala Gly Gly Leu Cys Ala
 225 230 235 240

Glu Ser Asn Pro Ala Gly Phe Leu Glu Ser Lys Ser Thr Thr Cys Thr
 245 250 255

Arg Phe Phe Gln Glu Pro Gly
 260

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1263 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGCAGCTCA TCAACCCCTT TGGAGAGGAT GATGATGATT TTGAGACCAA CTGGATTGTC	60
GACAGGAATT TGCAGGTGTC CCTGTTGGCT GTGGATGAGA TGCACCAGGA CCTGCCTCGG	120
ATGGAGCCGG ACATGTACTG GAATAAGCCC GAGCCACAGC CCCCCTACAC AGCTGCTTCC	180
GCCCAGTTCC GTCGAGCCTC CTTTATGGGC TCCACCTTCA ACATCAGCCT GAACAAAGAG	240
GAGATGGAGT TCCAGCCCAA TCAGGAGGAC GAGGAGGATG CTCACGCTGG CATCATTGGC	300
CGCTTCCTAG GCCTGCAGTC CCATGATCAC CATCCTCCCA GGGCAAATC AAGGACCAAA	360
CTACTGTGGC CCAAGAGGGA ATCCCTTCTC CACGAGGGCC TGCCCAAAAA CCACAAGGCA	420
GCCAAACAGA ACGTTAGGGG CCAGGAAGAC AACAAGGCCT GGAAGCTTAA GGCTGTGGAC	480
GCCTTCAAGT CTGCCCCACT GTATCAGAGG CCAGGCTACT ACAGTGCCCC ACAGACGCCC	540
CTCAGCCCCA CTCCCATGTT CTTCCCCCTA GAACCATCAG CGCCGTCAA GCTTCACAGT	600
GTACAGGCA TAGACACCAA AGACAAAAGC TTAAAGACTG TGAGTTCTGG GGCCAAGAAA	660
AGTTTTGAAT TGCTCTCAGA GAGCGATGGG GCCTTGATGG AGCACCAGAG AGTATCTCAA	720
GTGAGGAGGA AACTGTGGA GTTTAACCTG ACGGATATGC CAGAGATCCC CGAAAATCAC	780
CTCAAAGAAC CTTTGGAACA ATCACCACC AACATACACA CTACACTCAA AGATCACATG	840
GATCCTTATT GGGCCTTGGA AACAGGGAT GAAGCACATT CCTAACCTGC TTCCTAATGG	900
GGATGCTTCG CCAGCCAGGT CCTCACCTGT GTGTACACCA GCAGGACACT GATCCAGTCA	960
CAGCCATACA GCTGTCCACA CTGAAGAACA TGTCCTACAA CAGCCTGAAT CAAATGGCTA	1020
GCTTAATAGA TAAAAATCCC AGACTACTTC AGCCTTTAAT GCCTTTTATT CATAAAAACT	1080
GTGAAAGCTA GACTGAACCA TTGGAAACAT TTAATCAGA CTCTGGATTC AGAGTCGGGA	1140
ACCCTTAGTT CTATCTGAAT CCAAGACAGC CACACCTTAG TATACTGCCC AACTAATGA	1200

ATTY DOCKET NO.: GIN-6054CP

GTTTAATAAA TACAAATACT CGTTAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1260
 AAA 1263

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	His	Gln	Asp	Leu	Pro	Arg	Met	Glu	Pro	Asp	Met	Tyr	Trp	Asn	Lys	1	5	10	15
Pro	Glu	Pro	Gln	Pro	Pro	Tyr	Thr	Ala	Ala	Ser	Ala	Gln	Phe	Arg	Arg	20	25	30	
Ala	Ser	Phe	Met	Gly	Ser	Thr	Phe	Asn	Ile	Ser	Leu	Asn	Lys	Glu	Glu	35	40	45	
Met	Glu	Phe	Gln	Pro	Asn	Gln	Glu	Asp	Glu	Glu	Asp	Ala	His	Ala	Gly	50	55	60	
Ile	Ile	Gly	Arg	Phe	Leu	Gly	Leu	Gln	Ser	His	Asp	His	His	Pro	Pro	65	70	75	80
Arg	Ala	Asn	Ser	Arg	Thr	Lys	Leu	Leu	Trp	Pro	Lys	Arg	Glu	Ser	Leu	85	90	95	
Leu	His	Glu	Gly	Leu	Pro	Lys	Asn	His	Lys	Ala	Ala	Lys	Gln	Asn	Val	100	105	110	
Arg	Gly	Gln	Glu	Asp	Asn	Lys	Ala	Trp	Lys	Leu	Lys	Ala	Val	Asp	Ala	115	120	125	
Phe	Lys	Ser	Ala	Pro	Leu	Tyr	Gln	Arg	Pro	Gly	Tyr	Tyr	Ser	Ala	Pro	130	135	140	
Gln	Thr	Pro	Leu	Ser	Pro	Thr	Pro	Met	Phe	Phe	Pro	Leu	Glu	Pro	Ser	145	150	155	160
Ala	Pro	Ser	Lys	Leu	His	Ser	Val	Thr	Gly	Ile	Asp	Thr	Lys	Asp	Lys	165	170	175	
Ser	Leu	Lys	Thr	Val	Ser	Ser	Gly	Ala	Lys	Lys	Ser	Phe	Glu	Leu	Leu	180	185	190	
Ser	Glu	Ser	Asp	Gly	Ala	Leu	Met	Glu	His	Pro	Glu	Val	Ser	Gln	Val	195	200	205	
Arg	Arg	Lys	Thr	Val	Glu	Phe	Asn	Leu	Thr	Asp	Met	Pro	Glu	Ile	Pro	210	215	220	
Glu	Asn	His	Leu	Lys	Glu	Pro	Leu	Glu	Gln	Ser	Pro	Thr	Asn	Ile	His	225	230	235	240

ATTY DOCKET NO.: GIN-6054CP

Thr Thr Leu Lys Asp His Met Asp Pro Tyr Trp Ala Leu Glu Asn Arg
245 250 255

Asp Glu Ala His Ser
260

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTTGAGGGT TTTTGTGTTT TTGTTTTTTC TAGGATTTCA TTGTGATGTT TTGGTTTTGT	60
TTTTTGCTTT TTGTTTAAGT TGTGCTGACA CCAAACACAT CCAGTTTATA ATCAGTACAT	120
TGGAAAGCTG GTATTGATGT AGAACCAGTG CATAACTTTT TATGGGGTTT TGTTATTGGT	180
TTTTTTTTTG TAAAGTGTGA ATAAAAGGTA TGTTTACTCA TTTTTCCTGA ACACTGTGTT	240
GGTAATGTGC ATCATGACAA TTTCCAGTGA AGGTGAGCTG GAGCTGGTTG GACTAATGAG	300
ACTGAGGAAG CAGCTTTTCC TACGATCTGC ATTATGTAAT CACAGGTCCA GAGAGCTTTA	360
TGGAAGCGGG AGAGGAGGAG CACTTACTCA TGTTGTATTT GTTAATGGAG GATGTCATCT	420
TTTCATAGAT GCTGGAAC TA GAGTGCACTT GTTAGATGCT AAAGGTTTGA GCTTTACACA	480
AAATGTCTTC ATCTGTATTT GTTATTGTCT ACAATATATT TGAATTTGGG GCAGCATATT	540
AAGATGTAAT GCCCTGTTAT GTCTGGAAAA AACTTGTTTT GCTTCTTCCA GGCAAAGGGC	600
ATTTTGTGGA TCAGTTTGAA CAGCTTCTCC ACCTTATTTG GACAGTGATA AATTGAACCA	660
AGAGTGTAGA TTTACAAGTG TAACCTTCAA AAGAGGAAGA ACTATTTGGG GTCTGTAGGT	720
AATGAACAGT CACACCAAAA TAGACTATGA TGCTTTTGTT AAGAAAGGTT TCATGTTTTA	780
GATATTTTCC GTGCCTAAA TAATTTTCAA TAATCTATAA TCCCTAAAAT GCAATAAAAA	840
CTAGTATGTT TTCAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA	894

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Cys Ile Met Thr Ile Ser Ser Glu Gly Glu Leu Glu Leu Val Gly

ATTY DOCKET NO.: GIN-6054CP

1	5	10	15
Leu Met Arg	Leu Arg Lys Gln Leu Phe	Leu Arg Ser Ala	Leu Cys Asn
20	25	30	
His Arg Ser	Arg Glu Leu Tyr Gly	Ser Gly Arg Gly	Gly Ala Leu Thr
35	40	45	
His Val Val	Phe Val Asn Gly Gly	Cys His Leu Phe	Ile Asp Ala Gly
50	55	60	
Thr Arg Val	His Leu Leu Asp Ala Lys	Gly Leu Ser Phe	Thr Gln Asn
65	70	75	80
Val Phe Ile	Cys Ile Cys Tyr Cys	Leu Gln Tyr Ile	
85	90		

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 784 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGGCCGCAG GTCTACTTGT GGCGAGCAGT CCAGCACAGC CTCACAGTGC AGAGCATGAG	60
CTTTGGAGCC TGCCCCCACC CTAGCTTTGT GACCTTAAGT GAGCTACATA GCTTCTCATG	120
TGTAAACTAC TCATCATAAT GGTTCTGACC TCAGTGGTTT GTTGTGTTCT AGGAAATGAT	180
GCCAGTGAAT GCGTAGTCCC AGCCTCAGCA CAGGGGAGCC ACCTTGAAGC TCTCAAATAT	240
CACTGTTGTG AATACAGAGA GGGAAAACCA ACTGTAACGT GCCACCCAAA TTTTTCAGA	300
TTAATACATC ATTCATCAGA CTTCATTCGT GATCTCGAAG AGTGACATCA GTCTTCCTTG	360
GAATATGAAG AGAATTTCTT TGGTTCTTCT TTTGCATTTC TATTTGATTT ATTTTATTTT	420
ATTTTATTTT ATGTTTTTTG GTACAGAAAG CTCATTACTA GTCCTGTCCA GCAACGTGCC	480
TCTCCTGGCC CTAGAGTTCT TGGAAATAGC CCAGGCCAAA GAGAAGGCCT TTCTCCCCAT	540
GGTCAGCCAC ACGTTCCACA TGCGCACAGA GGAGTCTGAT GCCTCACAGG AGGGCGATGA	600
CCTACCCAAG TCCTCAGCAA ACACCAGCCA TCCAAGCAG GATGACAGCC CCAAGTCCTC	660
AGAAGAAACC ATCCAGCCCA AGGAGGGTGA CATCCCCAAG GCCCCAGAAG AAACCATCCA	720
ATCCAAGAAG GAGGACCTCC CCAAGTCCTC GGAAAAAGCC ATCCAGCCCA AAGAGAGTAA	780
CATC	784

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids

ATTY DOCKET NO.: GIN-6054CP

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met 1	Lys	Arg	Ile	Ser 5	Leu	Val	Leu	Leu	Leu 10	His	Phe	Tyr	Leu	Ile 15	Tyr
Phe	Ile	Leu	Phe 20	Tyr	Phe	Met	Phe	Phe 25	Gly	Thr	Glu	Ser	Ser 30	Leu	Leu
Val	Leu	Ser 35	Ser	Asn	Val	Pro	Leu 40	Leu	Ala	Leu	Glu	Phe 45	Leu	Glu	Ile
Ala 50	Gln	Ala	Lys	Glu	Lys	Ala 55	Phe	Leu	Pro	Met	Val 60	Ser	His	Thr	Phe
His 65	Met	Arg	Thr	Glu	Glu 70	Ser	Asp	Ala	Ser	Gln 75	Glu	Gly	Asp	Asp	Leu 80
Pro	Lys	Ser	Ser 85	Ala	Asn	Thr	Ser	His 90	Pro	Lys	Gln	Asp	Asp 95	Ser	Pro
Lys	Ser	Ser	Glu 100	Glu	Thr	Ile	Gln	Pro 105	Lys	Glu	Gly	Asp	Ile 110	Pro	Lys
Ala	Pro	Glu 115	Glu	Thr	Ile	Gln	Ser 120	Lys	Lys	Glu	Asp	Leu 125	Pro	Lys	Ser
Ser 130	Glu	Lys	Ala	Ile	Gln	Pro 135	Lys	Glu	Ser	Asn	Ile 140				

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAAAAAA AAAAA	75

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 939 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

ATTY DOCKET NO.: GIN-6054CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGAAGAAGTA GAAGCATCGA AAGCGTTGGA GAGGTGTTAC CGGAACGGCG GCGACAAGGG	60
TGTTCCCGAA CTAGAGTGGG GCATACATAA TCTTGCTGCT ATGCTTCGAA GCTGTAGTCT	120
GAATCAACCT AAGTTTTTAAA CAGAAGGTGA ACCTCTGAGA TAGAAAATCA AGTATATTTT	180
AAAAGAAGGG ATGTGGGATC AAGGAGGACA GCCTTGGCAG CAGTGGCCCT TGAACCAGCA	240
ACAATGGATG CAGTCATTCC AGCACCAACA GGATCCAAGC CAGATTGATT GGGCTGCATT	300
GGCCCAAGCT TGGATTGCCC AAAGAGAAGC TTCAGGACAG CAAAGCATGG TAGAACAACC	360
ACCAGGAATG ATGCCAAATG GACAAGATAT GTCTACAATG GAATCTGGTC CAAACAATCA	420
TGGGAATTTT CAAGGGGATT CAAACTTCAA CAGAATGTGG CAACCAGAAT GGGGAATGCA	480
TCAGCAACCC CCACACCCCC CTCCAGATCA GCCATGGATG CCACCAACAC CAGGCCCAAT	540
GGACATTGTT CCTCCTTCTG AAGACAGCAA CAGTCAGGAC AGTGGGGAAT TTGCCCCCTGA	600
CAACAGGCAT ATATTTAACC AGAACAATCA CAACTTTGGT GGACCACCCG ATAATTTTGC	660
AGTGGGGCCA GTGAACCAGT TTGACTATCA GGACCTCCAG GACCTCCAGC ACCTCCCCAG	720
AATCGAAGAG AAAGGCCATC ATCATTGAGG GATCGTCAGC GTTCACCTAT TGCACTTCCT	780
GTGAAGCAGG AGCCTCCACA AATTGACGCA GTAAACGCA GGACTCTTCC CGCTTGGATT	840
CGCGAAGGTC TTGAAAAAAT GGAACGTGAA AAGCAGAAGA AATTGGAGAA AGAAAGAATG	900
GAACAACAAC GTTCACAATT GTCCAAAAAA AAAAAAAAAA	939

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Trp Asp Gln Gly Gly Gln Pro Trp Gln Gln Trp Pro Leu Asn Gln	
1 5 10 15	
Gln Gln Trp Met Gln Ser Phe Gln His Gln Gln Asp Pro Ser Gln Ile	
20 25 30	
Asp Trp Ala Ala Leu Ala Gln Ala Trp Ile Ala Gln Arg Glu Ala Ser	
35 40 45	
Gly Gln Gln Ser Met Val Glu Gln Pro Pro Gly Met Met Pro Asn Gly	
50 55 60	
Gln Asp Met Ser Thr Met Glu Ser Gly Pro Asn Asn His Gly Asn Phe	
65 70 75 80	

ATTY DOCKET NO.: GIN-6054CP

Gln Gly Asp Ser Asn Phe Asn Arg Met Trp Gln Pro Glu Trp Gly Met
85 90 95

His Gln Gln Pro Pro His Pro Pro Pro Asp Gln Pro Trp Met Pro Pro
100 105 110

Thr Pro Gly Pro Met Asp Ile Val Pro Pro Ser Glu Asp Ser Asn Ser
115 120 125

Gln Asp Ser Gly Glu Phe Ala Pro Asp Asn Arg His Ile Phe Asn Gln
130 135 140

Asn Asn His Asn Phe Gly Gly Pro Pro Asp Asn Phe Ala Val Gly Pro
145 150 155 160

Val Asn Gln Phe Asp Tyr Gln Asp Leu Gln Asp Leu Gln His Leu Pro
165 170 175

Arg Ile Glu Glu Lys Gly His His His Ser Gly Ile Val Ser Val His
180 185 190

Leu Leu His Phe Leu
195

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGGAGAGCAG CCGGCAGCGC CTGGAGGCCC TGAGAGAGCT GCAATAAAGG AAGAAACAGA	60
ATATATGGAA CTTCTGGCAG CAGAAAAACA TCAAGTTGAA GCCCTTAAAA ATATGCAACA	120
TCAAAACCAA AGTTTATCCA TGCTTGACGA GATTCTTGAA GATGTAAGAA AGGCAGCGGA	180
TCGTCTGGAG GAAGAGATAG AGGAACATGC TTTTGACGAC AATAAATCAG TCAAGGGGGT	240
CAATTTTGAG GCAGTTCTGA GGGTGGAGGA AGAAGAGGCC AATTCTAAGC AAAATATAAC	300
AAAACGAGAA GTGGAGGATG ACTTGGGTCT TAGCATGCTG ATTGACTCCC AGAACAACCA	360
GTATATTTTG ACCAAGCCCA GAGATTCAAC CATCCCACGT GCAGATCACC ACTTTATAAA	420
GGACATTGTT ACCATAGGAA TGCTGTCCTT GCCTTGTTGGC TGGCTATGTA CAGCCATAGG	480
ATTGCCTACA ATGTTTGGTT ATATTATTTG TGGTGTACTT CTGGGACCTT CAGGACTAAA	540
TAGTATTAAG TCTATTGTGC AAGTGGAGAC ATTAGGAGAA TTTGGGGTGT TTTTACTCT	600
TTTCTTGTT GGCTTAGAAT TTTCTCCAGA AAAGCTAAGA AAGGTGTGGA AGATTCCTT	660
ACAAGGGCCG TGTTACATGA CACTGTTAAT GATTGCATTT GGCTTGCTGT GGGGGCATCT	720
CTTGCGGATC AAACCCACGC AGAGCGTCTT CATTTCCACG TGTCTGTCCT TGTCAGCAC	780

ACCCCTCGTG TCCAGGTTCC TCATGGGCAG TGCTCGGGGT GACAAAGAAG GCGACATTGA	840
CTACAGCACC GTGCTCCTCG GCATGCTGGT GACGCAGGAC GTGCAGCTCG GGCTCTTCAT	900
GGCCGTCATG CCGACTCTCA TACAGGCGGG CGCCAGTGCA TCTTCTAGCA TTGTCGTGGA	960
AGTTCTCCGA ATCCTGGTTT TGATTGGTCA GATTCTTTTTT TCACTAGCGG CGGTTTTTCT	1020
TTTATGTCTT GTTATAAAGA AGTATCTCAT TGGACCCTAT TATCGGAAGC TGCACATGGA	1080
AAGCAAGGGG AACAAAGAAA TCCTGATCTT GGAATATCT GCCTTTATCT TCTTAATGTT	1140
AACGGTCACG GAGCTGCTGG ACGTCTCCAT GGAGCTGGGC TGTTTCCTGG CTGGAGCGCT	1200
CGTCTCCTCT CAGGGCCCCG TGGTCACCGA GGAGATCGCC ACCTCCATCG AACCCATCCG	1260
CGACTTCCTG GCCATCGTTT TCTTCGCCTC CATAGGGCTC CACGTGTTCC CCACGTTTGT	1320
GGCGTACGAG CTCACGGTGC TGGTGTTCCCT CACCTTGTC A GTGGTGGTGA TGAAGTTTCT	1380
CCTGGCGGCG CTGGTCCTGT CTCTCATTCT GCCGAGGAGC AGCCAGTACA TCAAGTGGAT	1440
CGTCTCTGCG GGGCTTGCCC AGGTCAGCGA GTTTTCCTTT GTCCTGGGGA GCCGGGCGCG	1500
AAGAGCGGGC GTCATCTCTC GGGAGGTGTA CCTCCTTATA CTGAGTGTA CCACGCTCAG	1560
CCTCTTGCTC GCCCCGGTGC TGTGGAGAGC TGCAATCACG AGGTGTGTGC CCAGACCGGA	1620
GAGACGGTCC AGCCTCTGAT GGCTCGGAGA TGATGGACCG TGGAAGGGAA GCGTCTGTGG	1680
GGAGTGAGCG CTTAGATGGC CAGCAGCTGC TCCTTCTGGG AAGCTCGCAC CTTGGCAACA	1740
GAACAGCCCT CTAGCAGAGC GTCAGTGAGC TCGTGTTATC CCGGCTTTTA CAGAATATTC	1800
TTGTCCTATT TTAGAATTTT CCGGAGTAGT TTATTTGCAG TCTGTTGATT ATGTGCAGTA	1860
GACCCGGGAC ACTGCGTTTT ACCGATCACC TTGAATGTGG TGCCTGGATG TGCCTTTTTT	1920
TTTTTCCCT GAAATTATTA TTAATTTTCT ATKGKGAGTT CATCAGTTCA TAGTTTTTTT	1980
AGTAAAGAAG CAAATTAATA AGGCTTTTAA AAATGTACAA CTTCAGAATT ATAATCTGTT	2040
AGTCAAATAT TTGTTATTAA ACATTTCTGT AATATGAAGT TGTAATCCTG GCCGTGAGCT	2100
TGGAAGCTTA CTTTTGATTC TTAAAGCCTA TGTTTTCTAA AATGAGACAA ATACGGATGT	2160
CTATTTGCCT TTTATTGTAA CTTTAAATG AAATAATTTT ATGTCAATTT CTATTAGATA	2220
TATCACTTAA AATATTTGGT TTAAATCAC AAGAATATGT ATTCTTTAAT AAAGATAATT	2280
TATGATCATG GTATAATTAA TTGAAATTTA TTAAATCTG TTTTATTAA AAAAAAAAAA	2340
AAA	2343

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Glu	Leu	Leu	Ala	Ala	Glu	Lys	His	Gln	Val	Glu	Ala	Leu	Lys	Asn	1	5	10	15
Met	Gln	His	Gln	Asn	Gln	Ser	Leu	Ser	Met	Leu	Asp	Glu	Ile	Leu	Glu	20	25	30	
Asp	Val	Arg	Lys	Ala	Ala	Asp	Arg	Leu	Glu	Glu	Glu	Ile	Glu	Glu	His	35	40	45	
Ala	Phe	Asp	Asp	Asn	Lys	Ser	Val	Lys	Gly	Val	Asn	Phe	Glu	Ala	Val	50	55	60	
Leu	Arg	Val	Glu	Glu	Glu	Glu	Ala	Asn	Ser	Lys	Gln	Asn	Ile	Thr	Lys	65	70	75	80
Arg	Glu	Val	Glu	Asp	Asp	Leu	Gly	Leu	Ser	Met	Leu	Ile	Asp	Ser	Gln	85	90	95	
Asn	Asn	Gln	Tyr	Ile	Leu	Thr	Lys	Pro	Arg	Asp	Ser	Thr	Ile	Pro	Arg	100	105	110	
Ala	Asp	His	His	Phe	Ile	Lys	Asp	Ile	Val	Thr	Ile	Gly	Met	Leu	Ser	115	120	125	
Leu	Pro	Cys	Gly	Trp	Leu	Cys	Thr	Ala	Ile	Gly	Leu	Pro	Thr	Met	Phe	130	135	140	
Gly	Tyr	Ile	Ile	Cys	Gly	Val	Leu	Leu	Gly	Pro	Ser	Gly	Leu	Asn	Ser	145	150	155	160
Ile	Lys	Ser	Ile	Val	Gln	Val	Glu	Thr	Leu	Gly	Glu	Phe	Gly	Val	Phe	165	170	175	
Phe	Thr	Leu	Phe	Leu	Val	Gly	Leu	Glu	Phe	Ser	Pro	Glu	Lys	Leu	Arg	180	185	190	
Lys	Val	Trp	Lys	Ile	Ser	Leu	Gln	Gly	Pro	Cys	Tyr	Met	Thr	Leu	Leu	195	200	205	
Met	Ile	Ala	Phe	Gly	Leu	Leu	Trp	Gly	His	Leu	Leu	Arg	Ile	Lys	Pro	210	215	220	
Thr	Gln	Ser	Val	Phe	Ile	Ser	Thr	Cys	Leu	Ser	Leu	Ser	Ser	Thr	Pro	225	230	235	240
Leu	Val	Ser	Arg	Phe	Leu	Met	Gly	Ser	Ala	Arg	Gly	Asp	Lys	Glu	Gly	245	250	255	
Asp	Ile	Asp	Tyr	Ser	Thr	Val	Leu	Leu	Gly	Met	Leu	Val	Thr	Gln	Asp	260	265	270	
Val	Gln	Leu	Gly	Leu	Phe	Met	Ala	Val	Met	Pro	Thr	Leu	Ile	Gln	Ala	275	280	285	
Gly	Ala	Ser	Ala	Ser	Ser	Ser	Ile	Val	Val	Glu	Val	Leu	Arg	Ile	Leu				

290	295	300
Val Leu Ile Gly Gln Ile Leu Phe Ser Leu Ala Ala Val Phe Leu Leu		
305	310	315 320
Cys Leu Val Ile Lys Lys Tyr Leu Ile Gly Pro Tyr Tyr Arg Lys Leu		
	325	330 335
His Met Glu Ser Lys Gly Asn Lys Glu Ile Leu Ile Leu Gly Ile Ser		
	340	345 350
Ala Phe Ile Phe Leu Met Leu Thr Val Thr Glu Leu Leu Asp Val Ser		
	355	360 365
Met Glu Leu Gly Cys Phe Leu Ala Gly Ala Leu Val Ser Ser Gln Gly		
	370	375 380
Pro Val Val Thr Glu Glu Ile Ala Thr Ser Ile Glu Pro Ile Arg Asp		
	385	390 395 400
Phe Leu Ala Ile Val Phe Phe Ala Ser Ile Gly Leu His Val Phe Pro		
	405	410 415
Thr Phe Val Ala Tyr Glu Leu Thr Val Leu Val Phe Leu Thr Leu Ser		
	420	425 430
Val Val Val Met Lys Phe Leu Leu Ala Ala Leu Val Leu Ser Leu Ile		
	435	440 445
Leu Pro Arg Ser Ser Gln Tyr Ile Lys Trp Ile Val Ser Ala Gly Leu		
	450	455 460
Ala Gln Val Ser Glu Phe Ser Phe Val Leu Gly Ser Arg Ala Arg Arg		
	465	470 475 480
Ala Gly Val Ile Ser Arg Glu Val Tyr Leu Leu Ile Leu Ser Val Thr		
	485	490 495
Thr Leu Ser Leu Leu Leu Ala Pro Val Leu Trp Arg Ala Ala Ile Thr		
	500	505 510
Arg Cys Val Pro Arg Pro Glu Arg Arg Ser Ser Leu		
	515	520

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCAGCCCGG GCCATGCCGC ACGGCTGCTG ACCGCACGCA GGGGCCGGCC CCGAGGACAC	60
ATGCGGCGGC CTTTGCCGCC TCGCCCCTGA CCCTCTGCCC TGTTCTCCAT GTTGCAATTC	120
TCGTCAGTTT CTCGGGCGGT GTAGCTGCCG CTGCCACCAG AGCCGGCGGG GCATCGCGCT	180

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GCTCATT CAT CCGGCCGCAC TTTCTTTTCC GTTTCACCC ATCCCTTCCC ATTTCTTCT	240
CCCTTTCCCC GCCAGCTTCG CATCCATCTC CCCCACCCCG TAACCCCTCC TGCCTCCATC	300
CACCGGGGCT ATTGCCGCAA AAGA	324

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCTGAACATT TCAGAAATAC AGAAGTTGAA GCAGCAGCTT ATGCAGGTAG AGCGGGAAAA	60
GGCCATTCTT TTGGCCAACC TACAGGAGTC ACAGACACAG CTGGAACACA CCAAGGGGGC	120
ACTGACGGAG CAGCATGAGC GGGTGCACCG GCTCACAGAG CACGTCAATG CCATGAGGGG	180
CCTGCAAAGC AGCAAGGAGC TCAAGGCTGA GCTGGACGGG GAGAAGGGCC GGGACTCAGG	240
GGAGGAGGCC CATGACTATG AGGTGGACAT CAATGGTTTA GAGATCCTTG AATGCAAATA	300
CAGGGTGGCA GTAAGTGGG TGATTGATCT GAAAGCTGAA ATTAAGGCCT TAAAGGAGAA	360
ATATAATAAA TCTGTAGAAA ACTACACTGA TGAGAAGGCC AAGTATGAGA GTAAATCCA	420
GATGTATGAT GAGCAGGTGA CAAGCCTTGA GAAGACCACC AAGGAGAGTG GTGAGAAGAT	480
GGCCACATG GAGAAGGAGT TGCAAAGAT GACCAGCATA GCCAACGAAA ATCACAGTAC	540
CCTTAATACG	550

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Gln	Val	Glu	Arg	Glu	Lys	Ala	Ile	Leu	Leu	Ala	Asn	Leu	Gln	Glu
1				5					10					15	
Ser	Gln	Thr	Gln	Leu	Glu	His	Thr	Lys	Gly	Ala	Leu	Thr	Glu	Gln	His
			20					25					30		
Glu	Arg	Val	His	Arg	Leu	Thr	Glu	His	Val	Asn	Ala	Met	Arg	Gly	Leu
			35				40					45			
Gln	Ser	Ser	Lys	Glu	Leu	Lys	Ala	Glu	Leu	Asp	Gly	Glu	Lys	Gly	Arg

ATTY DOCKET NO.: GIN-6054CP

50	55	60
Asp Ser Gly Glu Glu Ala His Asp Tyr Glu Val Asp Ile Asn Gly Leu		
65	70	75 80
Glu Ile Leu Glu Cys Lys Tyr Arg Val Ala Val Thr Glu Val Ile Asp		
	85	90 95
Leu Lys Ala Glu Ile Lys Ala Leu Lys Glu Lys Tyr Asn Lys Ser Val		
	100	105 110
Glu Asn Tyr Thr Asp Glu Lys Ala Lys Tyr Glu Ser Lys Ile Gln Met		
	115	120 125
Tyr Asp Glu Gln Val Thr Ser Leu Glu Lys Thr Thr Lys Glu Ser Gly		
	130	135 140
Glu Lys Met Ala His Met Glu Lys Glu Leu Gln Lys Met Thr Ser Ile		
	145	150 155 160
Ala Asn Glu Asn His Ser Thr Leu Asn Thr		
	165	170

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTCCATGAGT GAATTCATCC AAGGGCACGG GTTCAGCAAG GAAAAAAGGT TAACCGTGGT	60
TCCACCAGCA AAAAGAGATT GTCAGCAGCC TGTGCTTCCG TACCGCCACA GTGTTACAA	120
CTAGCCGGGA GGCAAGACTG CCCAACTGTC AGTCCTGACA CAGCTCTCCC TGAGGAGCAG	180
CCACATTCCA GCTCCCAGTG CGCCCCTCTC CACTGTCTCT CCAAGCCTCC TCACCCCTAG	240
TCTTCATCTC CTGTGGACAA ACATCTGGGG TGGAAGTTTT GTAGCCACAC ACAGGATACT	300
GCCCAAGATC CAGCGGGTGT TTTCTTCTCG GTTGTTAGAT GTACAATTGG ATTAATGTCC	360
ATCGTTTTGG AAGACGAGAG AAAGTTGAGA AGAACACGAA GCACAGACCC TGATGTGATA	420
AAACATTTTG TGGTTTCTCT GAGTCACAGA TAAACTTCTG CCATCAAATG GCTACAGTTC	480
ATTTAAATTT AAAAAAAAAA AAAAA	505

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

ATTY DOCKET NO.: GIN-6054CP

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

GGATACTGTA ATAAATAGGA GACAGCTACA GTGATCCAAC TAAACCAACA GGGGATTTTC      60
ATCAGCACTT CCCTGGTGTA ATCATGGTAC AGATTATTAA AGACACGAAT GAATTTAAAA      120
CATTTTTGAC AGCTGCCGGA CACAACTCG CAGTGGTTCA ATTTTCTTCG AAACGGTGTG      180
GTCCCTGCAA AAGGATGTTT CCTGTTTTTC ATGAGCTGGC TGAAACTTGT CACATCAAAA      240
CAATACCCAC ATTCAGATG TTCAAGAAAA GCCAGAAGGT AACCTATTC TCAAGAATCA      300
AAAGAATAAT TTGCTGTTAT AGAAGTGGAT TCATGAGCAA CCTGATTTTT GAGTTTTGTG      360
GAGCCGATGC TAAAAAATTG GAAGCCAAGA CTCAAGAATT AATGTAAGCT GATCTCCAAG      420
GCAAAATACA CTTGTGACAT TTGAAAAGGC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      480
A                                                                                   481

```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met Val Gln Ile Ile Lys Asp Thr Asn Glu Phe Lys Thr Phe Leu Thr
1           5           10           15
Ala Ala Gly His Lys Leu Ala Val Val Gln Phe Ser Ser Lys Arg Cys
20           25           30
Gly Pro Cys Lys Arg Met Phe Pro Val Phe His Glu Leu Ala Glu Thr
35           40           45
Cys His Ile Lys Thr Ile Pro Thr Phe Gln Met Phe Lys Lys Ser Gln
50           55           60
Lys Val Thr Leu Phe Ser Arg Ile Lys Arg Ile Ile Cys Cys Tyr Arg
65           70           75           80
Ser Gly Phe Met Ser Asn Leu Ile Phe Glu Phe Cys Gly Ala Asp Ala
85           90           95
Lys Lys Leu Glu Ala Lys Thr Gln Glu Leu Met
100           105

```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCCAAAGAG GCCTATTCCT GTGTGCAATC AGTACCTTGA AGGCAGAACA TTCTGAATAA	60
AGTTGGAAAA AGAACAGCTT TGCTTTGCAA AGATTGATGA CAGACTGGTT CCTCAGAGGC	120
CTAGGCTACC CGTCACCCCT TTTTCCAGAG CGAGGGCCTG GAATGAAGGC AGTTTATCCT	180
CTGTCCCTGG AGCCTGGGGT TTGCTTTGGC TCCTTGAGGT GGAAGAGACT AAGAGGGCAG	240
CTGCCCAGAG CAGCTGTGTG TACCTGGCTC CTCTCAGGCT TCCTGATCCC TTCCATTGCA	300
CTGCGCCTTA TCCCTCAGCC AGCCAGACAG CCTCCCTGCT CCTGACCAGC AGATACGTTT	360
CGGAGTGGTT GGTGTGGTTT TTGTGATGAG GGCAGCACGT GGTGGCCAAG GTGGCAAGCT	420
GAGTCTCACA GGCTCACTCC CTCGTTGGTT CCCTGTGGGA ATGGTAGGCC AGGCCARTA	480
AGCCATGCCC CAACACGTCC TCTCCTCCGG AGGAAGGGCC AGCTGCCARC TGARTCAGCA	540
GCTAGTCCAT AGCACAGCCT TATAACTGTA AAGCCAGGCA TTGCCCATGA GCAGAGCTGG	600
AACCAGAGCT TCAGTCAGTA AGAGGGAGGA TTACCTTCAG GAGAAGGCAA GGAAGAAAAC	660
TGGCTGCTAT CTTTATAGTT CCACTGCCCT AACCAAGTGT CCACATTCTA AATGTGTAGT	720
GTCCATCCCT TATGTAATAG TGGTTTCCCG CCCAAAGTGA GACTTTCCTT TTAATTGGAG	780
AAGGGTATAG AGGTAGTCCA GGTGGGAACG CCAGAAGTGC TGATTGCCCA GCCATTGGGA	840
CCACCTGTTC TTGCCCCACT ACCCTCTAGT GGGAGGCCAA AGTAAAGGCT GGCTGGTGGG	900
TGTCTGTGGA TTGAGGATGT GGCAGGGACT GGTCCCTCCA CCTCCCTCTG GCCAAAGATG	960
GGCTTTGCCC GCTGTGTGCC TGTCACCACC CACCAGCAGT CATGCCCTGG GCTTCCCAA	1020
TGGAGAGGTA GCAGGCAACG TTTTAAAAA GAAAGAAAAC AGGAAACTGT ATTGTGTCGG	1080
GGGAGGCGGG AGGGAGATGA GGAAACGGTT TGGATTTTGT GTGTGGGAGG GTATTTTTTG	1140
GGGGTAGTTG TCTGTAACCT TCCTAAGTGC TTTTTCCT TTTCTTTTTT AAAGTAAGTT	1200
GCAGGCTTTG GCTTGAAAAA CCCCAGGGGG ATGGGGGGCA GAAACCTGAG GCTGCTGCCC	1260
TTTATCTGCC TTCACGGTAC TGTCCCCTTC CCCCAGCTCC TCCCTGACCC CATGGGCCAG	1320
GCCTCAGACC TTCCAGCTAA CCGCTTCCA TGAGCCACTA CTCTGATGTC AGCCTATAAC	1380
CAAAGGAGCT GGGGGGTCCA GGCCTGGTGA CCAACCTTTC TCAGCCCACT CAATCAGGGT	1440
GCTCCCCACC TGCAGGCAGG AGGCAACACC CTATCTGCTA CCATCAGCCC CTTCCAGAGC	1500
CCATCTGCCC CGCCCAGCCC TGCCCTGCCC AGCCATACCC TGCTCTGCCC CATCTGGGGG	1560
TGCCCTGCTC AGGGATGGGC TGGCAGGGCT GTACCCAGCC TCCCTGGTAA GCAGAGACTC	1620
AAGAAACCTC TGGGGTCCTG TTTTCTGGTC GTGTGATCCC AGGGGTGCAC ATGGGCCCCCT	1680

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TGGGTGTCTG AACAGAAGGG CATGGGAGGG AGGGCTGCAC CCCTGCAGTC TTACTCTGCT	1740
GGTGTAGCGG GCAGMTGCCC ACTCCCACCC CACCCTGCAC CGCGGGCTCC TGAGTCGGCA	1800
GATTAAGCAT TTTATAAATT GTATTTTAAA TACATGTTTT AAACTTGTCA AAAAAAAAAA	1860
AAAA	1864

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Val	Leu	Pro	Thr	Cys	Arg	Gln	Glu	Ala	Thr	Pro	Tyr	Leu	Leu	Pro	Ser	
1				5					10					15		
Ala	Pro	Ser	Arg	Ala	His	Leu	Pro	Arg	Pro	Ala	Leu	Pro	Cys	Pro	Ala	
			20					25					30			
Ile	Pro	Cys	Ser	Ala	Pro	Ser	Gly	Gly	Ala	Leu	Leu	Arg	Asp	Gly	Leu	
		35					40					45				
Ala	Gly	Leu	Tyr	Pro	Ala	Ser	Leu	Val	Ser	Arg	Asp	Ser	Arg	Asn	Leu	
	50					55					60					
Trp	Gly	Pro	Val	Phe	Trp	Ser	Cys	Asp	Pro	Arg	Gly	Ala	His	Gly	Pro	
65				70						75				80		
Leu	Gly	Cys	Leu	Asn	Arg	Arg	Ala	Trp	Glu	Gly	Gly	Leu	His	Pro	Cys	
			85						90					95		
Ser	Leu	Thr	Leu	Leu	Val											
			100													

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1041 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCCCTCGTA CTGATTTCCA TCGTTGCATT TACAACTGCT ACAAAAATGC CAGCACTCCA	60
TCGACATGAA GAAGAGAAAT TCTTCTTAAA TGCCAAAGGC CAGAAAGAAA CTTTACCCAG	120
CATATGGGAC TCACCTACCA AACAACTTTC TGTCGTTGTG CCTTCAAACA ATGAAGAAAA	180
ACGGTTGCCT GTGATGATGG ATGAAGCTCT GAGCTATGTA GAGAAGAGAC AGAAACGAGA	240

TCCTGCGTTC ACTTATGAAG TGATAGTAGT TGATGATGGC AGTAAAGATC AGACCTCAAA	300
GGTAGCTTTT AAATATTGCC AGAAATATGG AAGTGACAAA GTACGTGTGA TAACCCTGGT	360
GAAGAATCGT GGAAAAGGTG GAGCGATTAG AATGGGTATA TTCAGTTCTC GAGGAGAAAA	420
GATCCTTATG GCAGATGCTG ATGGAGCCAC AAAGTTTCCA GATGTTGAGA AATTAGAAAA	480
GGGGCTAAAT GATCTACAGC CTTGGCCTAA TCAAATGGCT ATAGCATGTG GATCTCGAGC	540
TCATTTAGAA AAAGAATCAA TTGCTCAGCG TTCTTACTTC CGTACTCTTC TCATGTATGG	600
GTTCCACTTT CTGGTGTGGT TCCTTTGTGT CAAAGGAATC AGGGACACAC AGTGTGGGTT	660
CAAATTATTT ACTCGAGAAG CAGCTTCACG GACGTTTTCA TCTCTACACG TTGAACGATG	720
GGCATTTGAT GTAGAACTAC TGTACATAGC ACAGTTCTTT AAAATTCCAA TAGCAGAAAT	780
TGCTGTCAAC TGGACAGAAA TTGAAGGTTT TAAATTAGTT CCATTCTGGA GCTGGCTACA	840
AATGGGTAAA GACCTACTTT TTATACGACT TCGATATTTG ACTGGTGCCT GGAGGCTTGA	900
GCAAACTCGG AAAATGAATT AGGTTGTTTG CAGTCTTCAG TTGTGTTCTT ATGCTTCAGT	960
GTCACATTTT ATTTTATTTG AAATAAAAT TTTAAGTAAA GCTGAAATAA ACTTCTTGTC	1020
ATTGTCAAAA AAAAAAAAAA A	1041

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Pro	Ala	Leu	His	Arg	His	Glu	Glu	Glu	Lys	Phe	Phe	Leu	Asn	Ala
1				5					10					15	
Lys	Gly	Gln	Lys	Glu	Thr	Leu	Pro	Ser	Ile	Trp	Asp	Ser	Pro	Thr	Lys
		20						25					30		
Gln	Leu	Ser	Val	Val	Val	Pro	Ser	Asn	Asn	Glu	Glu	Lys	Arg	Leu	Pro
		35					40					45			
Val	Met	Met	Asp	Glu	Ala	Leu	Ser	Tyr	Val	Glu	Lys	Arg	Gln	Lys	Arg
	50					55					60				
Asp	Pro	Ala	Phe	Thr	Tyr	Glu	Val	Ile	Val	Val	Asp	Asp	Gly	Ser	Lys
65				70					75					80	
Asp	Gln	Thr	Ser	Lys	Val	Ala	Phe	Lys	Tyr	Cys	Gln	Lys	Tyr	Gly	Ser
			85						90					95	
Asp	Lys	Val	Arg	Val	Ile	Thr	Leu	Val	Lys	Asn	Arg	Gly	Lys	Gly	Gly
		100						105					110		

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[illegible]

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- ```
(A) DESCRIPTION: /desc = "oligonucleotide"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CNCCATCGGG GAACACCAGA AAGAACACT

29

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TNTCTGGCAT ATCCGTCAGG TTAAACTCC

29

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CNCTGGTTCT ACATCAATAC CAGCTTTCC

29

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TNACAACAGT GATATTTGAG AGCTTCAAG

29

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CNGTAACACC TCTCCAACGC TTTCGATGC

29

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GNCAAGGACA GACACGTGGA AATGAAGAC

29

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ANGTCCACCT CATAGTCATG GGCCTCCTC

29

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TNTCAGCCAG CTCATGGAAA ACAGGAAAC

29

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CNTGGGAAGC GGTTAGCTGG AAGGTCTGA

29

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TNTCTTCTTC ATGTCGATGG AGTGCTGGC

29

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

Arg Val Lys Val Gln Leu Ala Leu Val Phe Phe Lys Asn Leu Ala Ser
 1 5 10 15
Ser Cys Thr Leu Asp Ser Ala Leu Asn Ala Ala Ser Tyr Tyr Asn Phe
 20 25 30
Thr Val Leu Lys Val Pro Arg Ser Met Thr Asp Pro Gln Asn Met Glu
 35 40 45
Phe Gln Val Pro Val Ile Leu Thr Ser Gln Ala Asn Ala Pro Leu Leu
 50 55 60
Ala Gly Asn Thr Cys Gln Asn Val Val Ser Gln Val Thr Tyr Glu Ile
65 70 75 80
Glu Thr Asn Gly Thr Phe Gly Ile Gln Lys Val Ser Val Ser Leu Gly
 85 90 95
Gln Thr Asn Leu Thr Val Glu Pro Gly Ala Ser Leu Gln Gln His Phe
 100 105 110
Ile Leu Arg Phe Arg Ala Phe Gln Gln Ser Thr Ala Ala Ser Leu Thr
 115 120 125
Ser Pro Arg Ser Gly Asn Pro Gly Tyr Ile Val Gly Lys Pro Leu Leu
 130 135 140
Ala Leu Thr Asp Asp Ile Ser Tyr Ser Met Thr Leu Leu Gln Ser Gln
145 150 155 160
Gly Asn Gly Ser Cys Ser Val Lys Arg His Glu Val Gln Phe Gly Val
 165 170 175
Asn Ala Ile Ser Gly Cys Lys Leu Arg Leu Lys Lys Ala Asp Cys Ser
 180 185 190
His Leu Gln Gln Glu Ile Tyr Gln Thr Leu His Gly Arg Pro Arg Pro
 195 200 205
Glu Tyr Val Ala Ile Phe Gly Asn Ala Asp Pro Ala Gln Lys Gly Gly
 210 215 220
Trp Thr Arg Ile Leu Asn Arg His Cys Ser Ile Ser Ala Ile Asn Cys
225 230 235 240
Thr Ser Cys Cys Leu Ile Pro Val Ser Leu Glu Ile Gln Val Leu Trp

```

|                                                                 |     |  |     |  |     |
|-----------------------------------------------------------------|-----|--|-----|--|-----|
|                                                                 | 245 |  | 250 |  | 255 |
| Ala Tyr Val Gly Leu Leu Ser Asn Pro Gln Ala His Val Ser Gly Val | 260 |  | 265 |  | 270 |
| Arg Phe Leu Tyr Gln Cys Gln Ser Ile Gln Asp Ser Gln Gln Val Thr | 275 |  | 280 |  | 285 |
| Glu Val Ser Leu Thr Thr Leu Val Asn Phe Val Asp Ile Thr Gln Lys | 290 |  | 295 |  | 300 |
| Pro Gln Pro Pro Arg Gly Gln Pro Lys Met Asp Trp Lys Trp Pro Phe | 305 |  | 310 |  | 315 |
| Asp Phe Phe Pro Phe Lys Val Ala Phe Ser Arg Gly Val Phe Ser Gln | 325 |  | 330 |  | 335 |
| Lys Cys Ser Val Ser Pro Ile Leu Ile Leu Cys Leu Leu Glu Leu Gly | 340 |  | 345 |  | 350 |
| Val Leu Asn Leu Glu Thr Met                                     | 355 |  |     |  |     |

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GTTGTACCAT TCTTGCCAAC TTCTGGGCTG GCAGTATGGA GTCATCTCCC TATCTTTCAT | 60  |
| TGCCTGTGTG AAATCTACTT TCTGAATTCT GCCATTTCCC TCTTCACACT GTCTCCTGGG | 120 |
| TTATCTTTGC TTCCTCACAT CCCTATCTCT CTTCTATAA ACTGGCTCCC GTCACATTCCA | 180 |
| TGATCCCTTC AGTGGCTTCT GAGCTGGTCT CCCTGACCCC AAAGCCTCAG CCTTCCAGTC | 240 |
| TCCCTACAAA ATCTCAGCAA GTTCATTTTA GGTTAAAATT TGGACATATT TTAAATACGG | 300 |
| CTCACCACTT CATGTGAAAA TGATGGCACC CTACCAAGCA GTTTGCAGAG TTACGGTAAC | 360 |
| TGTTTCATGC TAATGATGTT ATTCATCCAG TTACAATTTT CTCAAACTC CTTTGGGCAC  | 420 |
| TCTTTATTTT TAATCAAATT TTAAAGCCAA TATTTTATTT TGAGAATATG AATTAAATTG | 480 |
| GGAAATTCAT CCTTGTGGTA CAGTTTACAG ATTTTAAATG TTTACCCATT TATCCTGTTT | 540 |
| TTTGATATAT TAATTTCCCA TATAGCTCCA GAGTTATGTG ATATTATTTT TTTGCCAGTA | 600 |
| TATTAGAAAA TGATTAATTT CTCATGACCA ACTTCTGAAA AGAAAGACCC AATGCAAAAT | 660 |
| GCAATCTATT ACAATTATTT TTTTGAATAA AAAAGAATAT ATTATAGTTC TTTAACATTT | 720 |
| GATATTTTAA ATTTGACATA TTCTTGATAT TTGTAAGAAA TTTCCACTGA ATGAATTTTA | 780 |



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|                                                                     |      |
|---------------------------------------------------------------------|------|
| CACAATTCAG ATACTACCAA TTAACATAATT CTAGCCTAAA CAAATAACAT TATTTTTTAAA | 840  |
| TAACAAAATC TTTAAAAATA ATTTTCTATT TTGAACTTTT AGCCATAATG TAAGAAAATA   | 900  |
| AAATTTTCTA GCAGAATAAT CAAAGAGTGA AACAAAGTTC CAACATGTTT TTTCTTTGCA   | 960  |
| ATTAAACATG GCACTTTTAC AGTTATTTAT TATTCATATC AGTGCACTTA CCGACTTCAT   | 1020 |
| ATTTTCAAAT CAAAATACAG TGTTTTTCTC CAGTGAAATC CTTATTCTCA TGA CTGATAG  | 1080 |
| AAAACATTGC CAATTTTGAT ATTTCCAGAG TTAATGTTAA ATTATTTGAA AGAAAATTAT   | 1140 |
| TTAAAATAAT AAAAATAGAC ATTTCAAGAC TATTTCTTAT CACATAATTC AAAAAGTACT   | 1200 |
| TGGATCAAAT CCTACAGAGT TTCTCCACTA AAATTCTACT TGTGCAGAGG GCATTGAAAC   | 1260 |
| GCATGAAAAT CAACAGCAGC TTAGTTAGGT TAATTAATTC GGTTAATTAA GCACCTACTA   | 1320 |
| CATGCTCAGC TCTATGCTAG GTGTCATGAG GAATTTAAAAG GACATGTAAT GCACATTTTC  | 1380 |
| TGATTTCAAG GAGCTTTAAA TATTATTGTG TAGAAAAAGT TAACATCTAT GAAAATAGAA   | 1440 |
| GTGGGGCAAT TTTGTGCTTA ATTCCATGGT CCAGATACAT CAAAAAATCA ATGTGGGCTG   | 1500 |
| TCAAAGAAGG TTTCTTGATA GTCATGAGTC AGCCTGATTC TTGAAAGGAT ATGTGGAATA   | 1560 |
| TAAAATTTTA TTTATATTCC TTTTGAGAAA ATACTGAGAA AACCATCTTC CCTGGAAAAG   | 1620 |
| AGAACGTATT GTAAAGAAAG TACATGAAAT TGAAGGTTGA ATATCCAACA TCCCCCACAC   | 1680 |
| TGCCCCAGTG TCTCTGCTCC CTTACTGAGC CTTACTATTA TTCTTCATAG CCCTATCACT   | 1740 |
| ACCTAGTCTA GTATTCCTG AACTGTGTCA TCCACTAGAA TATGAGCATA ATGAGAGCAG    | 1800 |
| AGACTACACC TGTCGGTTCA GTATTCTATC CTCAGCACAT AGAATGGTAC CTGGCACATA   | 1860 |
| GCAGATGCTA AAATAAAATT TAAATGAATA AATTAATTCA ATCAACAAC TCAAGGTGTT    | 1920 |
| ATTATTACCT ACAACTATTG TTTACAAGAG GTATGCACCG TGGAAGATCC TGGAGACACA   | 1980 |
| ACAATGAATA AAGCCAAGCC AGTTCCTGCC CCCGTGGAGC TTGTAGTCAA GACATTGAAC   | 2040 |
| AAGTGATCAG AAAGATGTTG ACTGCTGCAG CAGAGGGTTG CAAGCTGCTC ATGAGTATAT   | 2100 |
| AACAAGTAGC CCTAACCAAA GCATTCTCTC CCTTGGTTTA ATGTCCACCC ATTGAGGTGA   | 2160 |
| CTGCTAAATA CTAATCCATG ACTCTATCCC TTGGCATTCA AACTCACACA TCCACTTACC   | 2220 |
| TGCCTCTCCA ACCTCATCTC CCTCCACTCA CAAGAGCCCA TCATATTATT CATCAAAATG   | 2280 |
| AAACTGCACC CAGTTCTTCT GAACATATTA CCTTACAAAA CTTTCATTTA TGCCTGGTGA   | 2340 |
| CTCTCATCAG GCATTCAAAA GCTTTCCCTC AGTGCTTCAG GGCTCTTCCT TTTCTTCCCT   | 2400 |
| TTATACATAC ACCTTTATGT ATCTTCATAC GTACCCTGCA TAACCTCATA TATCTTAGCA   | 2460 |
| TTTACCATAT TCTGTTGAAA AACTGTTTCC ATTTCTCTTT ACTTACTAGA ATGTAAACAG   | 2520 |
| ATGCACAATG TTGAGAAAAT GAAAAGTGAC AACTTTGTTT ACAAGTTTAG AAATTATCAG   | 2580 |
| ATTCTCACYT AAGCTCTAGT CTCTGTAAAG TCCACAAC TA CTYAATAAAA GTGAAGAAAA  | 2640 |

ATGTTAACAG AGAGGGAGGA ATCAAAAACA AAGAACTATT TAAAAA AAAA

2696

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Met Thr Leu Ser Leu Gly Ile Gln Thr His Thr Ser Thr Tyr Leu Pro
1 5 10 15

Leu Gln Pro His Leu Pro Pro Leu Thr Arg Ala His His Ile Ile His
20 25 30

Gln Asn Glu Thr Ala Pro Ser Ser Ser Glu His Ile Thr Leu Gln Asn
35 40 45

Phe His Leu Cys Leu Val Thr Leu Ile Arg His Ser Lys Ala Phe Pro
50 55 60

Gln Cys Phe Arg Ala Leu Pro Phe Leu Pro Phe Ile His Thr Pro Leu
65 70 75 80

Cys Ile Phe Ile Arg Thr Leu His Asn Leu Ile Tyr Leu Ser Ile Tyr
85 90 95

His Ile Leu Leu Lys Asn Cys Phe His Phe Ser Leu Leu Thr Arg Met
100 105 110

```

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3614 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

CGCGCTAACT GTGCTCCTCC GGGGCCCTCC GCCTGCTCCC AGCCATGGTG GCCTGGCGCT 60
CGGCGTTCCT TGTCTGCCTC GCTTTCCTCT TGGCCACCCT GGTCCAGCGA GGATCTGGGG 120
ACTTTGATGA TTTTAACCTG GAGGATGCAG TGAAAGAAAC TTCCTCAGTA AAGCGATCAC 180
TGTAAGGATG ACATGGGAGG AGCCATGTGA AGCACTCAGC ACAGTCCTTG GAACAAGAGC 240
CATGGGACCA CACCACCACC ACCACAACCA ATAGGCCAGG AACCACCAGA GCTCCGGCAA 300
AACCTCCAGG TAGTGGATTG GACTTGGCTG ATGCTTTGGA TGATCAAGAT GATGGCCGCA 360
GGAAACCGGG TATAGGAGGA AGAGAGAGAT GGAACCATGT AACCACCACG ACCAAGAGGC 420

```

|                                                                   |      |
|-------------------------------------------------------------------|------|
| CAGTAACCAC CAGAGCTCCA GCAAATACTT TAGGAAATGA TTTTGACTTG GCTGATGCCC | 480  |
| TGGATGATCG AAATGATCGA GATGATGGCC GCAGGAAACC AATTGCTGGA GGAGGAGGTT | 540  |
| TTTCAGACAA GGATCTTGAA GACATAGTAG GGGGTGGAGA ATACAAACCT GACAAGGGTA | 600  |
| AAGGTGATGG CCGGTACGGC AGCAATGACG ACCCTGGATC TGGCATGGTG GCAGAGCCTG | 660  |
| GCACCATTGC CGGGGTGGCC AGCGCCCTGG CCATGGCCCT CATCGGTGCC GTCTCCAGCT | 720  |
| ACATCTCCTA CCAGCAGAAG AAGTTCTGCT TCAGCATTCA GCAGGGTCTC AACGCAGACT | 780  |
| ACGTGAAGGG AGAGAACCTG GAAGCCGTGG TATGTGAGGA ACCCCAAGTG AAATACTCCA | 840  |
| CGTTGCACAC GCAGTCTGCA GAGCCGCCGC CGCCGCCCGA ACCAGCCCGG ATCTGAGGGC | 900  |
| CCTGTCCAGC TGCAGGCATG CACAATGGTG CCACCGCTTG TCACCCGGCT CCCCCACCC  | 960  |
| CTTCATTTGG ACCCGCAGCT GCTGTGCTGC TCTGTGCCGT CGGCTCCTTG TTGGTCTGAG | 1020 |
| TTTCCCGGAT GAGCTCTGGG TGTTTGTGAG TTTGGTTTCT CTGCCCTGCC CCAAGCGTGC | 1080 |
| TGAGACTTGG TGCCGAAATT CAAGAGCCAG CTCTGATAGA AAGCCAGCAC CAGCCTCGGG | 1140 |
| AGCTGCTGAG CCACCAACTC CCAAAGCCAG CCTGCCTCCA GCTTTACTGA GCACAGGATG | 1200 |
| CGGGGGCCAA GATGATGCTG AGGCCTGATG ACATTTATGC TTAGGGGACA AGAGTTTGAA | 1260 |
| CTCAAGGGAC TGTGACCCCT GCACACTGGA GTGGCTCATT GTGGCAGGTT TCTGCCAATA | 1320 |
| GACAGCCCCT GACAGTGGCC TCAAGGAGCT GCAGGTGGGG GGCTCAGCCT GCACCCACTT | 1380 |
| GGAGCCCCTG CAAGGAGCGA ACCGGTCAGC ACCAAGTAAC ACCACACACA CGCAGCACCC | 1440 |
| AGGATGATGG TTCACTTCA GTCTTCCCCA TCCCAGGTTT TATGTTGCTG GGCTTCCGGA  | 1500 |
| GAGCCGGTCC AAGCGGAGGC TTTCAGTGAT TTAAGTACAA ACATGCATCT CGTGATAGTC | 1560 |
| CTGCCTTGAG AGCTTAGGAA TCTTCCGGAT AAGTATGAAG CAATTCGTAG GCCTGTTTCC | 1620 |
| CATCTGATTC CATAGGGGGC TGGGTGTGGC TTCGGGTTGA CATGAGAAAG GTCTTTAGCA | 1680 |
| ATCATTTCTG CACCGGAGAT GAGTTTTATC CTGTGTTGGG GAGAGGTGCT CACCCTCCAC | 1740 |
| CCTGTGTCCC TGTTTTGGTA GCAAGAGTGA CCGATGTCAA GAACGAGCAT CAAAGCCAGA | 1800 |
| ATCCTGCTTG TTTGCTTAAA AATGTAATTG GGGGCGGCGG GGGAGGAGAG GGGAAAGAGA | 1860 |
| CATTGCTTG GTTTAGTGAA ACGCAGGTGA CTTTGTAGCT CTGTGGTCAG CCTACTTGTC  | 1920 |
| TGCTCTGAGG GAGAGTGCCT GGGGAGCCAT GCTCACCGTG GCAAACACAG GAACCCCATG | 1980 |
| ACTCGCCCCT CACCTGGCGT GGAGCTGCCT GGTTCGGGCT GGAGCAGAGC TGGTTTCCTG | 2040 |
| GAATGTTCTT TTGGCCCACA TATGGTTCTG TCCCGGTGAG CTCTGTTGTC AGAGGCTCAC | 2100 |
| GGGACAGAAC CACATGCTAG GGTCTAGGGC CCCTGTCTAC TGATAGTCAG TTTGCTGTGT | 2160 |
| CAGAAAGCAC TTCTGAAAGC AGATATGAGT CACCAGACAG GCAGGATCTT ACAAACCTCA | 2220 |

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|                                                                   |      |
|-------------------------------------------------------------------|------|
| CGGGCCTCTT TGGTCTGCAT GATGGCCCCA TCGTTCAT AGGCTGTCCA CTGAGCGGGA   | 2280 |
| TTGTCTGCTG AGTGGGATGA GCCAACTCCA GTTCTTAAG GAAACCACTG GAATCTGCAG  | 2340 |
| CCCCACATG CATCTGTCTA ACGCATGCCT CGTGTTTCGTT TTGCAAACAT GCCTGTGGTG | 2400 |
| GAGGGTGGTC AGTTGTAGCC CTGTGCGTCT CAAGGCTGCC TTGTGAGGCC ATTCCCAGTG | 2460 |
| CGTGCCCTTG AGCTCCTTAC CACCCCTTTT CCTGCTCGGC CCTTTAATCC CTGACAGACC | 2520 |
| TGGACTGTGT GGCTGAAGGG GGACCTGCAG CACTGCAGAA ATGCCTCTGC GTGGTGCCAT | 2580 |
| GAAGGAAAGA AACCTTGGCC TGGTCTCGAG AAGCTTCCCA TGCTTCAGGA AGTTAGTAAG | 2640 |
| GGTGGGGTGG CTTGCAGGAT TGGCCTGTTT CCAGGGCCTC CCACACTCAT TGGCCAGATT | 2700 |
| GTGAACTTTG TCAGGCTTGT CCCTCCCTGA TACCAAGTAT GTCGAGAACC GATGGCCCCA | 2760 |
| CCCTCTGGCT GGTGCTGGGC CGGAGGTGGC TATGGAGGAT TTTGGCATGC GTGGCCTGTC | 2820 |
| GCCACCTGGA CAGCGTGACC TCAGGGGTTG TCCACTTTAC CTTTATGGTG AGGCCTGTGC | 2880 |
| GATGGCTAAG TCCTTGAAAC CCTAGAGCTG TGACGTAGAA TATGTGCTGT CTGTGAGACC | 2940 |
| GTGTTCCCAG GAGCACTGAC TGCAGTTGAG AGAGACCCAT TTTGCTCTCC CTTACCGCCC | 3000 |
| CCCGCCCCGG GTGCTTTCTG CACAAAGCCT AGAGCCTGGC ACTCAAGCCC ACCGGTGGCA | 3060 |
| GCTCCTAGTG ACTGGACATG CCTGGAAGAC CCCTCAGCCT TCTGTTTGCA GAACGTTTAT | 3120 |
| TTCAGGAGCT TCTCCTTCCC ACAGACATCT TACACTTGCT CGACACTGCC ACCTGCAGAA | 3180 |
| GCCTGGCGGG CTCTGGTCAC CATGTGTCTA TCTGAAGGTT GCACTGGCCA GCATGGGCCT | 3240 |
| GTCCCAAGCG AGAGGGGAGA CACAGTGGAC TGAAAGGACT GGTTGAAAGT GGCCAATCTC | 3300 |
| TGTCAGCTTA ATTTGGCAGA GAAAATTTGT AACAACTCTG AGCACATGCT GGGTGAAGTC | 3360 |
| ACAGCTCAAG GAAAGATAAA GCTGGGCGGA AGGAGGTGTG CGTGGCTTCT GGGGTGGGAC | 3420 |
| CCAGAGGGGA GGCTCTGGGA CAGGGGCTGG GGTTCAGTGC CAGGGCCCTG AGGAAGAAAT | 3480 |
| GGGGACTGAT CTCAAAATTC CAGAATTCCC TGTACATCTG TTCACGTGCT TGTGTCCAGG | 3540 |
| TGTGACTTGT AAAGTGTCTA GTGTTTGCAT TAAATAAAAT GGCACCGAGC AAAAAAAAAA | 3600 |
| AAAAAAAAAA AAAA                                                   | 3614 |

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 229 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Val Lys His Ser Ala Gln Ser Leu Glu Gln Glu Pro Trp Asp His Thr

|                                                                 |                                             |     |     |
|-----------------------------------------------------------------|---------------------------------------------|-----|-----|
| 1                                                               | 5                                           | 10  | 15  |
| Thr Thr Thr Thr Thr                                             | Asn Arg Pro Gly Thr Thr Arg Ala Pro Ala Lys |     |     |
| 20                                                              | 25                                          | 30  |     |
| Pro Pro Gly Ser Gly Leu Asp Leu Ala Asp Ala Leu Asp Asp Gln Asp |                                             |     |     |
| 35                                                              | 40                                          | 45  |     |
| Asp Gly Arg Arg Lys Pro Gly Ile Gly Gly Arg Glu Arg Trp Asn His |                                             |     |     |
| 50                                                              | 55                                          | 60  |     |
| Val Thr Thr Thr Thr Lys Arg Pro Val Thr Thr Arg Ala Pro Ala Asn |                                             |     |     |
| 65                                                              | 70                                          | 75  | 80  |
| Thr Leu Gly Asn Asp Phe Asp Leu Ala Asp Ala Leu Asp Asp Arg Asn |                                             |     |     |
| 85                                                              | 90                                          | 95  |     |
| Asp Arg Asp Asp Gly Arg Arg Lys Pro Ile Ala Gly Gly Gly Gly Phe |                                             |     |     |
| 100                                                             | 105                                         | 110 |     |
| Ser Asp Lys Asp Leu Glu Asp Ile Val Gly Gly Gly Glu Tyr Lys Pro |                                             |     |     |
| 115                                                             | 120                                         | 125 |     |
| Asp Lys Gly Lys Gly Asp Gly Arg Tyr Gly Ser Asn Asp Asp Pro Gly |                                             |     |     |
| 130                                                             | 135                                         | 140 |     |
| Ser Gly Met Val Ala Glu Pro Gly Thr Ile Ala Gly Val Ala Ser Ala |                                             |     |     |
| 145                                                             | 150                                         | 155 | 160 |
| Leu Ala Met Ala Leu Ile Gly Ala Val Ser Ser Tyr Ile Ser Tyr Gln |                                             |     |     |
| 165                                                             | 170                                         | 175 |     |
| Gln Lys Lys Phe Cys Phe Ser Ile Gln Gln Gly Leu Asn Ala Asp Tyr |                                             |     |     |
| 180                                                             | 185                                         | 190 |     |
| Val Lys Gly Glu Asn Leu Glu Ala Val Val Cys Glu Glu Pro Gln Val |                                             |     |     |
| 195                                                             | 200                                         | 205 |     |
| Lys Tyr Ser Thr Leu His Thr Gln Ser Ala Glu Pro Pro Pro Pro Pro |                                             |     |     |
| 210                                                             | 215                                         | 220 |     |
| Glu Pro Ala Arg Ile                                             |                                             |     |     |
| 225                                                             |                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1077 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AATCGGGAGT CCCAACAGCG TTAGGTTTTT TTTTTGTTT GTTTGTTTGT TTTGTTTTTT  | 60  |
| TCCAACCCTC TTTCGGATGG ACGGGGGAAA GAGAGAAAGA AAAACGAGGG AAAATCAACA | 120 |
| AAATGTGCGA TGCAAAGAGT CGATTTTCGC GGGGTTTGTC AACTTCGCCA CTGCCGCACG | 180 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| CGAATCGACG TCGTCACGTG ACGGTCTGCC TCCGCCCTTA TTAAGTCTCA GCCCAGCGGC | 240  |
| GGTTTCCAGG ACCTCAGACT TTTTGCCGAG GCGGCAGTCC CTAGACGAAG CGAAGGAGGC | 300  |
| GGCGCCTGCC CCGCCCACAA GAGCTGCCGC GCGCGGGTGT TATAGCTCCA CCCCATCTGC | 360  |
| AAAGGAAGGG GGAGCGGAAA GAGCGGGATC TAGCGTGGGA TAAAAGTGGG ACTACTACAG | 420  |
| TGTAAGTGGG CATGCGCCCC TCCTAGAAAT GATGGGAATG CAAAAGCCCT TGACTGCTCC | 480  |
| AGGACTCGAG GGATCCTCGG TGCCAGGATG CTGGGTCAAG CGCTCCGCCG GGACAGAGGA | 540  |
| CTCATACCAG GGAAATGGAG CCCAGCCTCG TGATAAACTA CGACCCAAGC TGGGGGAGGA | 600  |
| ACCTAGTTTT CGAAAGGAAA ATAATATGCG CAAGCTTTAA CTGAGCAGTG GGATGGTCTT | 660  |
| AAATACCAA GGAATGACTT TAAATCTTGC TGGATGGGAC TGCCACTCAC CGCTAGAAAT  | 720  |
| CGGGGATCAA CAGCAAACTC TGGATGACCC TGTAACCACA TCTCCAGTTC AGCCCGGCGA | 780  |
| GGGGCATCCT CACCCACCAG CAAAGTACCA TCCACCTTAT TGATGACAGG GATCCGGGTC | 840  |
| TCCAGGTCCA CATCAAGGTG ATTAGGCTCT TCCATGCACT CCACCTCCAG CTGCAAACCC | 900  |
| AGAATCCACC CCCATGAGCA CATACTCTTC TTTGGGGGAG GGAGGGAGGG GGAGCAGGGC | 960  |
| CAATGGTAGT CATGAAATGA CTCTAGTATT TTCCATTCCC CCAGTCCCAC TGCCTTCATC | 1020 |
| AATTATTGGG AATAAAAAGA CAATCTAATC GTCAAAAAAA AAAAAAAAAA AAAAAAA    | 1077 |

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asp | Gly | Gly | Lys | Arg | Glu | Arg | Lys | Thr | Arg | Glu | Asn | Gln | Gln | Asn |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Val | Arg | Cys | Lys | Glu | Ser | Ile | Phe | Ala | Gly | Phe | Val | Asn | Phe | Ala | Thr |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Ala | Arg | Glu | Ser | Thr | Ser | Ser | Arg | Asp | Gly | Leu | Pro | Pro | Pro | Leu |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Thr | Leu | Ser | Pro | Ala | Ala | Val | Ser | Arg | Thr | Ser | Asp | Phe | Leu | Pro |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Arg | Arg | Gln | Ser | Leu | Asp | Glu | Ala | Lys | Glu | Ala | Ala | Pro | Ala | Pro | Pro |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Thr | Arg | Ala | Ala | Ala | Arg | Gly | Cys | Tyr | Ser | Ser | Thr | Pro | Ser | Ala | Lys |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |

Glu Gly Gly Ala Glu Arg Ala Gly Ser Ser Val Gly  
100 105

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TAAGAATTAA AAATGTCATC CAAACAAGAA ATAATGAGTG ACCAGCGGTT TAGACGGGTT  | 60  |
| GCAAAGGACC CGAGATTTTG GGAAATGCCA GAAAAGGATC GAAAAGTCAA AATTGACAAG  | 120 |
| AGATTTTCGAG CCATGTTTCA TGACAAGAAG TTCAAGTTGA ACTATGCCGT GGATAAAAGA | 180 |
| GGGCGCCCCA TTAGCCATAG CACTACAGAG GATTTGAAGC GTTTTTACGA CCTTTCAGAT  | 240 |
| TCTGATTCCA ATCTCTCTGG TGAAGATAGC AAAGCATTGA GTCAAAAGAA AATAAAGAAG  | 300 |
| AAAAAAACCC AGACTAAAAA AGAAATCGAT TCAAAAAATC TAGTTGAGAA AAAGAAAGAA  | 360 |
| ACCAAGAAGG CTAATCACAA GGGTTCTGAA AATAAACTG ATTTAGATAA TTCTATAGGA   | 420 |
| ATTAAAAAAA TGAAAACCTC ATGTAAATTT AAGATAGATT CAAACATAAG TCCGAAGAAG  | 480 |
| GATAGCAAAG AATTTACACA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA  | 540 |
| AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAA               | 588 |

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ser Ser Lys Gln Glu Ile Met Ser Asp Gln Arg Phe Arg Arg Val |  |
| 1 5 10 15                                                       |  |
| Ala Lys Asp Pro Arg Phe Trp Glu Met Pro Glu Lys Asp Arg Lys Val |  |
| 20 25 30                                                        |  |
| Lys Ile Asp Lys Arg Phe Arg Ala Met Phe His Asp Lys Lys Phe Lys |  |
| 35 40 45                                                        |  |
| Leu Asn Tyr Ala Val Asp Lys Arg Gly Arg Pro Ile Ser His Ser Thr |  |
| 50 55 60                                                        |  |
| Thr Glu Asp Leu Lys Arg Phe Tyr Asp Leu Ser Asp Ser Asp Ser Asn |  |
| 65 70 75 80                                                     |  |

Leu Ser Gly Glu Asp Ser Lys Ala Leu Ser Gln Lys Lys Ile Lys Lys  
85 90  
Lys Lys Thr Gln Thr Lys Lys Glu Ile Asp Ser Lys Asn Leu Val Glu  
100 105 110  
Lys Lys Lys Glu Thr Lys Lys Ala Asn His Lys Gly Ser Glu Asn Lys  
115 120 125  
Thr Asp Leu Asp Asn Ser Ile Gly Ile Lys Lys Met Lys Thr Ser Cys  
130 135 140  
Lys Phe Lys Ile Asp Ser Asn Ile Ser Pro Lys Lys Asp Ser Lys Glu  
145 150 155 160  
Phe Thr Gln

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GTATATTTTG GTTTACTTAC TCCTCTATTT CAGAAATTGA AAAAGATCCC CAAGGATCTG | 60  |
| TTACTACTGC ATTTCTTCT TGCTCTGTCT ACAGCCTAGG CCAACTAGTC AGGGTCTGGA  | 120 |
| CATGCATCTC CTAAAGGAAG AACTGTGTAG CACCATTGAT CACAATGTAA CATTTCATG  | 180 |
| CTGCATTAAG GGTGTCTCTC TCTAATCATG ATTGTACCTG TCTCTTCCTG GGTAAAGGGA | 240 |
| GATTTTTTTT TTTAATGTG TAAAGAATTG ATGCSAGCCA GGAACATGTC TGTAGTCCCA  | 300 |
| GCTACTTGGG CACACGCCTG TAGTCCMSCG CCACTCGAGC ACACACCTGT AGTACCAGCT | 360 |
| ACTCTGGAGG CTGAGGCAGG AGGATCACTT GAGCCCAGGA GATTAAGACT GTAGTATACT | 420 |
| ATGATCGTGC CTGTGGCTAG CCACTGTGCT CCAGCCTGGG CAACACCATC GTAAAAATAA | 480 |
| ATAAATAAAT AAATAAATTG GGGAGGACAG CCTCACTGGT ATCAGACTTA CAGGACCAGA | 540 |
| TAGACAAGAT GGGTATAAGG GGAGCTGAAG TCTGTGTTCA TATGAGGAAG AGAAGACCAA | 600 |
| GCCCTGGGAC TTTGGCTGAA TTCCTCCGTG GGGCTGGACG GCAGTGATCT CCTGTTCCCT | 660 |
| ATGTGTAAAC AAAGATTCCA GGGCGTGGTT TTGCACTCCT GTTGTACTCT TTTAGAGGTG | 720 |
| GAAAAGAGGT GGATACTGAG ATCTAAGAGG AAAGGATAGT CATTACGTT CTGAGATATG  | 780 |
| CGCTCTCTCT ATTGTTCTCG WACACAAAGG GATAGTCTCT TTTCTGGAGC TGATGTCCCT | 840 |
| GCTTGAGGT TAGCCCCAAA ACATGGCTCT TGTATTGTTT TAAGAGAAAA GGCTTTCATT  | 900 |



|                                                                   |      |
|-------------------------------------------------------------------|------|
| TTGGTTCTTC TGATTGGTGT TACCTACTGC CTAATATGTG TTCATTTTTT GACAGAGAGG | 960  |
| CAGACTATTG AAAAAGTCTG TGTGAACAGA GAGCAGTTCA TTAAGCCCAT TGCTTTCAGT | 1020 |
| AATGTGGCCT TGACCCCTTC TGCTTCCCCC TTCTCCCATG GAGCATGGCA GGGCTTGATT | 1080 |
| ATTTAGAGTC CATACTGCA AGCCATTGAG AGACTTGTTT GCTCAAATGC AAGTTTGCTC  | 1140 |
| AAAAACAGGT CCTGAAGGCT TGCTTAGGAT TACAGGGATG CTGGGTAAGA ACACCGTTCC | 1200 |
| TCTCTCTCGC TGGAGAAATC CCTGTTTCTC TGAATCCCTT TGTGATCCTC ACAGTAATGT | 1260 |
| ATTCTGTGCC ACTGTAGGAC ACAAGGCTCT GGGCCAGTAG AACAGGCAGA GAGGTGACAC | 1320 |
| TGGGCAGCAA GCTGAGAGCT CTTTCTAAAT GGAGTGAAGG AATTCAGTGG CCTAGTTTCG | 1380 |
| CCATTCTCTA ATGAGAAACC AAGGCCAGGC TGAAAAGTGC AATTAGATGT GGTGGATTGT | 1440 |
| GGTAACGGCC TCCAGATAAA GGGGTTATCC CTGTGGAAGT GACTTTTCCC CATTTGATCC | 1500 |
| CTTTTCAACT CTAAATGGCC AGGCCAGAG CAGAAGAAGG GTTGGGTCTG GAAGGAAGGC  | 1560 |
| TCCAAAGGAT GAAAGCTTCT CCCTGATCAT AAGGAAGTGC ATCTTTATAG AATTGTTGTG | 1620 |
| CATAATGTCA GTAAATCCCT CTCATTGAC AAGGGACTGG ATTCATCTTG CCTTGAGACG  | 1680 |
| GGCCAGTAGT TATCAGTGAG TCAAAGCAAA GTGAAAGTTT CAGGAGATGG GACCAATGGT | 1740 |
| GCAATGCTCG CCATAACAAA ATTCCTTAAA AATAAAAAAG CTAATGTTAT AGCAACAAAA | 1800 |
| AAAGACTGAA GCAAACCAC ACTGAAATGC ATCCCACTCC AGGAGAGGAA TTCTTAGCGT  | 1860 |
| AACACTCTAA ATAAATGGAA GGAATCATCA CCTTCCTTAT TTTACCCCTG CCTTGTTTAC | 1920 |
| CAGGCTGCCC AGTGCTTACC ATGCAGAAAG CAGTCAGCTG TACTCTGGAA GTTCTGTTC  | 1980 |
| TTCTTTCCTG GGGCTTAGGA TATTCTGGGA GCTGTCTGAG CCTTGTGCCT AAGGCTTATC | 2040 |
| AGGTGATATA ATCTTCCTGT TCTGGGCTGC TTGCTGGAGG AATAGGAAGT GACATTTATA | 2100 |
| AGACACAGGC GGTGTGAGCA TCCATGTGTG GTCTTGGTCT AAACCAGCTC TTGAACAGGT | 2160 |
| TAAAGCAAAC AGCAATAACA AAACAAAAAC TACTGATGCT GAGCGTTTTG ATCCTAGTAA | 2220 |
| TATTTCAAAT ATTGTCCTTC TGCATATGTT CTATCCATAT TTGATTCCAA TATACATTAT | 2280 |
| TAAGCTTTCT TGGGTACTAT TTTGCTGGGG CTCTTGCCTG AAGGTGGTAC CTGTCTCATG | 2340 |
| ATCCTTAAAA GAGAGAGGCT TTTTTCATCC AAAGCTGTAG TGTTGGGAAC TGGGGTGGGA | 2400 |
| GAGGCACTTT TTGGAATTCT GAAAGAATCA TATCTGTGTA TATACATACT GAGTGGGGAA | 2460 |
| GGATGGGGGT TGGCAGGGGT TGAGGGAGGT GGGAACAAAC AGTGAGTATG GGAACAGGCA | 2520 |
| GTCACCTCGA GTGTGGGAGG TCACCTGGGT CCGTCGTCTT CCTTCTGTAT GGTGTTGGGT | 2580 |
| TTATGTACAC ACTATAACAC TTCCTGTGTG AGTTCATGTA CCTGTCTGTG AGTGCTTTGG | 2640 |
| TGTATTGAGC CTCAGTACAC TCCAAGGGCA TTAAAGTCAA GAACTAGAAC CTGGAAAAAA | 2700 |
| AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 2760 |

AAAAAAAAAA AAA

2773

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

Met Arg Ser Leu Tyr Cys Ser Arg Thr Gln Arg Asp Ser Leu Phe Ser
 1 5 10 15
Gly Ala Asp Val Pro Ala Trp Arg Leu Ala Pro Lys His Gly Ser Cys
 20 25 30
Ile Val Leu Arg Glu Lys Ala Phe Ile Leu Val Leu Leu Ile Gly Val
 35 40 45
Thr Tyr Cys Leu Ile Cys Val His Phe Leu Thr Glu Arg Gln Thr Ile
 50 55 60
Glu Lys Val Cys Val Asn Arg Glu Gln Phe Ile Lys Pro Ile Ala Phe
 65 70 75 80
Ser Asn Val Ala Leu Thr Pro Ser Ala Ser Pro Phe Ser His Gly Ala
 85 90 95
Trp Gln Gly Leu Val Ile
 100

```

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

GGAAACATTA TGGATCTGTG GAGCTGCTTA TTTCCAGTGA TGCTGATGGA GCCATCCAAA 60
GGGCTGGAAG ATTCAGAGTG GAAAATGGCT CTTAGATGA GAATGCAACT GCCCTGCCTG 120
GTACTTGGCG AAGAACAGAC GTGCACTTAG AGAACCCAGA ATACCACACC AGATGGTATT 180
TCAAATATTT TTTAGGACAA GTCCATCAGA ACTACATTGG AAACGATGCC GAGAAGAGCC 240
CTTTCTTCTT GTCCGTGACC CTTTCTGACC AAAACAATCA ACGTGTCCCT CAATACCGTG 300
CAATTCTTTG GAGAAAAACA GGTACCCAGA AAATATGCCT TCCCTACAGT CCCACAAAAA 360
CTCTTTCTGT GAAGTCCATC TTAAGTGCCA TGAATCTGGA CAAATTTGAG AAAGGCCCCA 420

```

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GGGAAATTTT TCATCCTGAA ATACAAAAGG ACTTGCTGGT TCTTGAAGAA CAAGAGGGCT  | 480  |
| CTGTGAATTT CAAGTTTGGG GTTCTTTTTG CCAAAGATGG GCAGCTCACT GATGATGAGA  | 540  |
| TGTTCAAGAA TGAAATTGGA AGCGAGCCTT TTCAAAAATT TTTAAATCTT CTGGGTGACA  | 600  |
| CAATCACTCT AAAGGGCTGG ACGGGCTACC GTGGCGGTCT GGATACCAAA AATGATACCA  | 660  |
| CAGGGATACA TTCAGTTTAT ACTGTGTACC AAGGGCATGA GATCATGTTT CATGTTTCCA  | 720  |
| CCATGTTGCC ATATTCCAAA GAGAACAAAC AGCAGGTGGA AAGGAAACGC CACATTGGAA  | 780  |
| ACGATATCGT CACCATTTGTG TTCCAAGAAG GAGAGGAATC TTCTCCTGCC TTTAAGCCTT | 840  |
| CCATGATCCG CTCCCCTTT ACACATATTT TTGCCTTAGT GAGATACAAT CAACAAAATG   | 900  |
| ACAATTACAG GCTGAAAATA TTTTCAGAAG AGAGCGTACC ACTCTTTGGC CCTCCCTTGC  | 960  |
| CAACTCCACC AGTGTTTACA GACCACCAGG AATTCAGGGA CTTTTTGCTA GTGAAATTAA  | 1020 |
| TTAATGGTGA AAAAGCCACT TTGGAAACCC CAACATTTGC CCAGAAACGT CGGCGTACCC  | 1080 |
| TGGATATGTT GATTAGATCT TTACACCAGG ATTTGATGCC AGATTTGCAT AAGAACATGC  | 1140 |
| TTAATAGACG ATCTTTTAGT GATGTCTTAC CAGAGTCACC CAAGTCAGCG CGGAAGAAAG  | 1200 |
| AGGAGGCCCG CCAGGCGGAG TTTGTTAGAA TAGGGCAGGC ACTAAACTG AAATCCATTG   | 1260 |
| TGAGAGGGGA TGCTCCATCA AGCTTGGCAG CTTCAGGGAT CTGTAAAAA GAGATGACCT   | 1320 |
| TCCATCAGTG CCCGTGTTTG ACAGAACTCT GCCAGTGAAG CAAATGCATG TGCTTGAGAC  | 1380 |
| CCTGGACCTT CTGGTTCTCA GAGCAGACAA AGGAAAAGAT GCTCGCCTCT TTGTCTTCAG  | 1440 |
| GCTAAGTGCT CTGCAAAAGG GCCTTGAGGG GAAGCAGGCT GGGAAGAGCA GGTCTGACTG  | 1500 |
| CAGAGAAAAC AAGTTGGAGA AAACAAAAGG CTGCCACCTG TATGCTATTA AACTCACCA   | 1560 |
| CAGCAGAGAG CTGAGGATTG TGGTTGCAAT TCGGAATAAA CTGCTTCTGA TCACAAGAAA  | 1620 |
| ACACAACAAG CCAAGCGGGG TCACCAGCAC CTCATTGTTA TCTCCCCTGT CTGAGTCACC  | 1680 |
| TGTTGAAGAA TTCCAGTACA TCAGGGAGAT CTGTCTGTCT GACTCTCCCA TGGTGATGAC  | 1740 |
| CTTAGTGGAT GGGCCAGCTG AAGAGAGTGA CAATCTCATC TGTGTGGCTT ATCGACACCA  | 1800 |
| ATTTGATGTG GTGAATGAGA GCACAGGAGA AGCCTTCAGG CTGCACCACG TGGAGGCCAA  | 1860 |
| CAGGGTTAAT TTTGTTGCAG CTATTGATGT GTACGAAGAT GGAGAAGCTG GTTTGCTGTT  | 1920 |
| GTGTTACAAC TACAGTTGCA TCTATAAAAA GGTTCGCCCC TTTAATGGTG GCTCTTTTTT  | 1980 |
| GGTTCAACCT TCTGCGTCAG ATTTCCAGTT CTGTTGGAAC CAGGCTCCCT ATGCAATTGT  | 2040 |
| CTGTGCTTTC CCGTATCTCC TGGCCTTCAC CACCGACTCC ATGGAGATCC GCCTGGTGGT  | 2100 |
| GAACGGGAAC CTGGTCCACA CTGCAGTCGT GCCGCAGCTG CAGCTGGTGG CCTCCAGGTC  | 2160 |
| GGATATATAC TTCACAGCAA CTGCAGCTGT GAATGAGGTC TCATCTGGAG GCAGCTCCAA  | 2220 |

GGGGGCCAGT GCCCGAAATT CTCCTCAGAC ACCCCCGGGC CGAGATACTC CAGTATTTCC 2280  
 TTCTTCCCTG GGGGAAGGTG AAATTCAATC AAAAAATCTG TACAAGATTC CACTTAGAAA 2340  
 CCTCGTGGGC AGAAGCATCG AACGACCTCT GAAGTCACCC TTAGTCTCCA AGGTCATCAC 2400  
 CCCACCCACT CCCATCAGTG TGGGCCTTGC TGCCATTCCA GTCACGCACT CCTTGTCCCT 2460  
 GTCTCGCATG GAGATCAAAG AAATAGCAAG CAGGACCCGC AGGGAACACT TGGGCCTCTC 2520  
 GGATGAAGGT GGACCCAAGT CAGAAGGAGC GCCAAAGGCC AAATCAAAAC CCCGGAAGCG 2580  
 GTTAGAAGAA AGCCAAGGAG GCCCCAAGCC AGGGGCAGTG AGGTCATCTA GCAGTGACAG 2640  
 GATCCCATCA GGCTCCTTGG AAAGTGCTTC TACTTCCGAA GCCAACCCCTG AGGGGCACTC 2700  
 AGCCAGCTCT GACCAGGACC CTGTGGCAGA CAGAGAGGGC AGCCCGGTCT CCGGCAGCAG 2760  
 CCCCTTCCAG CTCACGGCTT TCTCCGATGA AGACATTATA GACTTGAAGT AACAGAGTTG 2820  
 AATCTCATTT GCCATCTTTA GTTTTCTTAT GGAGGTTTAT ACTCTTTAAA CAGTTCTGAT 2880  
 GTAATTTCTC AACAAAATGT GGCTTTTAGC CTGTCAGTGA TCTATTGGAC CAAACCTTCT 2940  
 GCACACTCGG CCAGTTCCTT CTCCAATGTC CGGTGCCATC TTTCTGACC TTTGTTTCTT 3000  
 TCTGTTTCTC AACCATCAGT CCCCTTGTA TAAAGGTGGT AGATTTCATT GAGGTTTTAG 3060  
 ATTGAACTT TGAATAAATC AAAAATACTC ATTCTTAAAA AAAAAAAAAA AAAAAAAAAA 3119

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Asn Leu Asp Lys Phe Glu Lys Gly Pro Arg Glu Ile Phe His Pro  
 1 5 10 15  
 Glu Ile Gln Lys Asp Leu Leu Val Leu Glu Glu Gln Glu Gly Ser Val  
 20 25 30  
 Asn Phe Lys Phe Gly Val Leu Phe Ala Lys Asp Gly Gln Leu Thr Asp  
 35 40 45  
 Asp Glu Met Phe Ser Asn Glu Ile Gly Ser Glu Pro Phe Gln Lys Phe  
 50 55 60  
 Leu Asn Leu Leu Gly Asp Thr Ile Thr Leu Lys Gly Trp Thr Gly Tyr  
 65 70 75 80  
 Arg Gly Gly Leu Asp Thr Lys Asn Asp Thr Gly Ile His Ser Val  
 85 90 95  
 Tyr Thr Val Tyr Gln Gly His Glu Ile Met Phe His Val Ser Thr Met

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 100                                                             | 105 | 110 |
| Leu Pro Tyr Ser Lys Glu Asn Lys Gln Gln Val Glu Arg Lys Arg His |     |     |
| 115                                                             | 120 | 125 |
| Ile Gly Asn Asp Ile Val Thr Ile Val Phe Gln Glu Gly Glu Glu Ser |     |     |
| 130                                                             | 135 | 140 |
| Ser Pro Ala Phe Lys Pro Ser Met Ile Arg Ser His Phe Thr His Ile |     |     |
| 145                                                             | 150 | 155 |
| Phe Ala Leu Val Arg Tyr Asn Gln Gln Asn Asp Asn Tyr Arg Leu Lys |     |     |
| 165                                                             | 170 | 175 |
| Ile Phe Ser Glu Glu Ser Val Pro Leu Phe Gly Pro Pro Leu Pro Thr |     |     |
| 180                                                             | 185 | 190 |
| Pro Pro Val Phe Thr Asp His Gln Glu Phe Arg Asp Phe Leu Leu Val |     |     |
| 195                                                             | 200 | 205 |
| Lys Leu Ile Asn Gly Glu Lys Ala Thr Leu Glu Thr Pro Thr Phe Ala |     |     |
| 210                                                             | 215 | 220 |
| Gln Lys Arg Arg Arg Thr Leu Asp Met Leu Ile Arg Ser Leu His Gln |     |     |
| 225                                                             | 230 | 235 |
| Asp Leu Met Pro Asp Leu His Lys Asn Met Leu Asn Arg Arg Ser Phe |     |     |
| 245                                                             | 250 | 255 |
| Ser Asp Val Leu Pro Glu Ser Pro Lys Ser Ala Arg Lys Lys Glu Glu |     |     |
| 260                                                             | 265 | 270 |
| Ala Arg Gln Ala Glu Phe Val Arg Ile Gly Gln Ala Leu Lys Leu Lys |     |     |
| 275                                                             | 280 | 285 |
| Ser Ile Val Arg Gly Asp Ala Pro Ser Ser Leu Ala Ala Ser Gly Ile |     |     |
| 290                                                             | 295 | 300 |
| Cys Lys Lys Glu Met Thr Phe His Gln Cys Pro Cys Leu Thr Glu Leu |     |     |
| 305                                                             | 310 | 315 |
|                                                                 |     | 320 |
| Cys Gln                                                         |     |     |

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1592 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GACTTTTATA AAAAAGTCAA GCAGTACAAA AGGGTGTAAA GTGAAGTTAC TGTCCTTCCC | 60  |
| CTCCATAAAC CCCCTGACCT TGGGAACTG TTGTTAACAG TTAAGTGGGT AACTTTTCAG  | 120 |
| ATATTTTGTA TGCATGTACA AATGTGAGTA TCTAATGTAA AAAAATCAAA CCAAGATAAA | 180 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GTGTAAACTG CTATGATGGA ATCCTGCCTT GTTCTGCTAT TAGTCTTCTG TTTAATAATC  | 240  |
| AGCTTTGGTA TTAGGACAGT GGTAGGAAGA AGCCAGTATG TCCTGCAACA TAATTTGTGG  | 300  |
| TTCTGGACTG GTCAGGATTT CCTGAATGCA GCCTTTATCT GGAAGCTCTG CCCTTCTCCA  | 360  |
| TCTGGGATAC GCTTTTTTCAT CCATCAAAAC TGTCATCTCC CTCTGTGAAG CCTTCCCTGA | 420  |
| CTATTCTCTG TCCCTCTTTC CTCTCTTCCC ACAAACACAA CTGTGTACGC GTGTCACCAA  | 480  |
| AGAGTTAATC GTGCTTTTCT CTGTGCTACT TTTATACSTA GTATATGGTC CATTGTTTTG  | 540  |
| CACTTAATAC ACTCTCTTGT AATGATTTGT TTACATGTCA GTCTCCCAGC CAGACTGAGA  | 600  |
| GCTCACCAAG GGCAGAAGCC GTGTTTTGTT TACTGCTGTA TTCCTGGTAC CTGGTACAAT  | 660  |
| GCTTGGCATA CAGTTGGATG AACGGGAAAG TAATCTGAGC TGCCGGTGCT GTGGCAGTGC  | 720  |
| AAAGTGGGCA TATTTGTGCC CTTGGACCAG ATGTAGCCCT TGATGCATTT TGCAGGAACA  | 780  |
| CGGCTTAGTT ATTGTTTACT TTGAAGCCCT TTTGCCTCTA CTCTCTCCCA TATATCTTCT  | 840  |
| CCTGACAGGG TGAAGTCACC TATAGCATTT CCTAGTGTAT GGAAGTATTA ATTTCTTTCT  | 900  |
| TTACTGGAAG AGCTACTAGC TTTTCTTCAT ACAGTTTCCT CTGCTCCAGT TTCATAAGTT  | 960  |
| TCTTTTTTGGC TTGTATCTGT TTAGGATCAG GTGATATGGC TTCATTTCTC ATGACTGAAG | 1020 |
| CCCGGCAACA TAACACTGAA ATTCGAATGG CAGTCAGCAA AGTGGCTGAT AAAATGGATC  | 1080 |
| ATCTCATGAC TAAGGTTGAA GAGTTACAGA AACATAGTGC TGGCAATTCC ATGCTTATTC  | 1140 |
| CTAGCATGTC AGTTACAATG GAAACAAGCA TGATTATGAG CAACATCCAG CGAATCATTC  | 1200 |
| AGGCCAAGGT GACAGAGGAG TTAGCAGCGG CCACTGCACA GKTCTCTCAT CTGCAGCTGA  | 1260 |
| AAATGACTTG CTCACCAAAA AAAGGAAACA GAGCTGCAGA TGCAGCTGAC AGAAAGCCTG  | 1320 |
| AAGGAGACAG ATCTTCTCAG GGGCCAGCTC ACCAAAGTGC AGGCAAAGCT CTCAGAGCTC  | 1380 |
| CAAGAAACYT CTGAGCAAGC ACAGTCCAAA TTCAAAAGTG AAAAGCAGAA CCGGAAACAA  | 1440 |
| CTGGAACTCA AGGTGACATC CCTGGAGGAG GAACTGACTG ACCTTCGAGT TGAGAAGGAG  | 1500 |
| TCCTTGGAAG AGGTAAGCTC TACAACCCAG TTTGCCAGAA TTAGCTGTTT AATAAACATT  | 1560 |
| TTTATTTTCC TTTTACAAAA AAAAAAAAAA AA                                | 1592 |

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Glu Val Leu Ile Ser Phe Phe Thr Gly Arg Ala Thr Ser Phe Ser

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Ser Tyr Ser Phe Leu Cys Ser Ser Phe Ile Ser Phe Phe Leu Ala Cys | 20  | 25  | 30  |
| Ile Cys Leu Gly Ser Gly Asp Met Ala Ser Phe Leu Met Thr Glu Ala | 35  | 40  | 45  |
| Arg Gln His Asn Thr Glu Ile Arg Met Ala Val Ser Lys Val Ala Asp | 50  | 55  | 60  |
| Lys Met Asp His Leu Met Thr Lys Val Glu Glu Leu Gln Lys His Ser | 65  | 70  | 75  |
| Ala Gly Asn Ser Met Leu Ile Pro Ser Met Ser Val Thr Met Glu Thr | 85  | 90  | 95  |
| Ser Met Ile Met Ser Asn Ile Gln Arg Ile Ile Gln Ala Lys Val Thr | 100 | 105 | 110 |
| Glu Glu Leu Ala Ala Ala Thr Ala Gln Xaa Ser His Leu Gln Leu Lys | 115 | 120 | 125 |
| Met Thr Cys Ser Pro Lys Lys Gly Asn Arg Ala Ala Asp Ala Ala Asp | 130 | 135 | 140 |
| Arg Lys Pro Glu Gly Asp Arg Ser Ser Gln Gly Pro Ala His Gln Ser | 145 | 150 | 155 |
| Ala Gly Lys Ala Leu Arg Ala Pro Arg Asn Xaa                     | 165 | 170 |     |

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1694 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGGAAACGGG AAGCCGCTGC AAGTCCACCG CCTCAGCTAC CCAGATTGGG ATCTGCCCAG | 60  |
| GCCCGCTTTA TGGACTAGTG TGGGCGGCAG GCTCCTTTCC GTCCCTGCCC TGCTGTACCC | 120 |
| CGCTCCTTGG AGACCCCTG TATCCCTCCC GCAAGGTGGA ATCCGCAGGC TGGAGGCTCC  | 180 |
| CAGGGGAGGC AAACGCCTGG CCCTGCCCTG CCCCACGCCG CACCATGACC CTCCTGCTGC | 240 |
| TGCCCTTCT GCTGGCCTCT CTGCTCGCGT CCTGCTCCTG TAACAAAGCC AACAAGCACA  | 300 |
| AGCCATGGAT TGAGGCAGAG TACCAGGGCA TCGTCATGGA GAATGACAAC ACGGTCCTAC | 360 |
| TGAATCCACC ACTCTTTGCC TTGGACAAGG ATGCCCCGCT GCGCTATGCA GGTGAGATCT | 420 |
| GCGGCTTCCG GCTCCATGGG TCTGGGGTGC CCTTTGAGGC TGTGATCCTT GACAAGGCGA | 480 |
| CAGGAGAGGG GCTGATCCGG GCCAAGGAGC CTGTGGACTG CGAGGCCAG AAGGAACACA  | 540 |

CCTTCACCAT CCAGGCCTAT GACTGTGGCG AGGGCCCCGA CGGGGCCAAC ACCAAGAAGT 600  
 CCCACAAGGC CACTGTGCAT GTGCGGGTCA ACGATGTGAA CGAGTTTGCC CCAGTGTTTG 660  
 TGGAACGGCT GTATCGTGCG GCTGTGACAG AGGGGAAGCT GTACGATCGC ATCCTGCGGG 720  
 TGGAAGCCAT TGACGGTGAC TGCTCCCCC AGTACAGCCA GATCTGCTAC TATGAGATTC 780  
 TCACACCCAA CACCCCTTTC CTCATTGACA ATGACGGGAA CATTGAGAAC ACAGAGAAGC 840  
 TGCAGTACAG TGGTGAGAGG CTCTATAAGT TTACAGTGAC AGCTTATGAC TGTGGGAAGA 900  
 AGCGGGCAGC AGATGATGCT GAGGTGGAGA TTCAGGTGAA GCCCACCTGT AAACCCAGCT 960  
 GGCAAGGCTG GAACAAAAGG ATCGAATATG CACCAGGTGC TGGGAGCTTG GCTTTGTTCC 1020  
 CTGGTATCCG CCTGGAGACC TGTGATGAAC CACTCTGGAA CATTCAGGCC ACCATAGAGC 1080  
 TGCAGACCAG CCATGTGGCC AAGGGCTGTG ACCGTGACAA CTACTCAGAG CGGGCGCTGC 1140  
 GGAAACTCTG TGGTGCTGCC ACTGGGGAGG TGGATCTGTT GCCCATGCCT GGCCCCAATG 1200  
 CCAACTGGAC AGCAGGACTC TCGGTGCACT ACAGCCAGGA CAGCAGCCTG ATCTACTGGT 1260  
 TCAATGGCAC CCAGGCTGTG CAGGTGCCCC TGGGTGGCCC CAGTGGGCTG GGCTCTGGGC 1320  
 CCCAGGACAG CCTCAGTGAC CACTTCACCC TGTCTTCTG GATGAAGCAT GGCGTAACTC 1380  
 CCAACAAGGG CAAGAAGGAA GAGGAAACCA TCGTATGTAA CACTGTCCAG AATGGTGAGC 1440  
 CTCCCCTCCA GGCCTAGCC AGAGGGGGAA ACTGGCTTCT TGTCCCGCCT CTGTCACTGC 1500  
 CCAGTGTGTG ACTGTGAACA GGTCACTTCC CCTCTCTTCA TTTGTGAGGT GCAAGTGCCA 1560  
 GGTGTGATAT GCCTTGATTC TGTGCTTTAT CCCCAACATG ACATGTTGGA TCGTAAAAAA 1620  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1680  
 AAAAAAAAAA AAAA 1694

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 428 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Thr Leu Leu Leu Leu Pro Leu Leu Leu Ala Ser Leu Leu Ala Ser  
 1 5 10 15  
 Cys Ser Cys Asn Lys Ala Asn Lys His Lys Pro Trp Ile Glu Ala Glu  
 20 25 30  
 Tyr Gln Gly Ile Val Met Glu Asn Asp Asn Thr Val Leu Leu Asn Pro  
 35 40 45



Pro Leu Phe Ala Leu Asp Lys Asp Ala Pro Leu Arg Tyr Ala Gly Glu  
50 55 60

Ile Cys Gly Phe Arg Leu His Gly Ser Gly Val Pro Phe Glu Ala Val  
65 70 75 80

Ile Leu Asp Lys Ala Thr Gly Glu Gly Leu Ile Arg Ala Lys Glu Pro  
85 90 95

Val Asp Cys Glu Ala Gln Lys Glu His Thr Phe Thr Ile Gln Ala Tyr  
100 105 110

Asp Cys Gly Glu Gly Pro Asp Gly Ala Asn Thr Lys Lys Ser His Lys  
115 120 125

Ala Thr Val His Val Arg Val Asn Asp Val Asn Glu Phe Ala Pro Val  
130 135 140

Phe Val Glu Arg Leu Tyr Arg Ala Ala Val Thr Glu Gly Lys Leu Tyr  
145 150 155 160

Asp Arg Ile Leu Arg Val Glu Ala Ile Asp Gly Asp Cys Ser Pro Gln  
165 170 175

Tyr Ser Gln Ile Cys Tyr Tyr Glu Ile Leu Thr Pro Asn Thr Pro Phe  
180 185 190

Leu Ile Asp Asn Asp Gly Asn Ile Glu Asn Thr Glu Lys Leu Gln Tyr  
195 200 205

Ser Gly Glu Arg Leu Tyr Lys Phe Thr Val Thr Ala Tyr Asp Cys Gly  
210 215 220

Lys Lys Arg Ala Ala Asp Asp Ala Glu Val Glu Ile Gln Val Lys Pro  
225 230 235 240

Thr Cys Lys Pro Ser Trp Gln Gly Trp Asn Lys Arg Ile Glu Tyr Ala  
245 250 255

Pro Gly Ala Gly Ser Leu Ala Leu Phe Pro Gly Ile Arg Leu Glu Thr  
260 265 270

Cys Asp Glu Pro Leu Trp Asn Ile Gln Ala Thr Ile Glu Leu Gln Thr  
275 280 285

Ser His Val Ala Lys Gly Cys Asp Arg Asp Asn Tyr Ser Glu Arg Ala  
290 295 300

Leu Arg Lys Leu Cys Gly Ala Ala Thr Gly Glu Val Asp Leu Leu Pro  
305 310 315 320

Met Pro Gly Pro Asn Ala Asn Trp Thr Ala Gly Leu Ser Val His Tyr  
325 330 335

Ser Gln Asp Ser Ser Leu Ile Tyr Trp Phe Asn Gly Thr Gln Ala Val  
340 345 350

Gln Val Pro Leu Gly Gly Pro Ser Gly Leu Gly Ser Gly Pro Gln Asp  
355 360 365

Ser Leu Ser Asp His Phe Thr Leu Ser Phe Trp Met Lys His Gly Val  
 370 375 380  
 Thr Pro Asn Lys Gly Lys Lys Glu Glu Glu Thr Ile Val Cys Asn Thr  
 385 390 395 400  
 Val Gln Asn Gly Glu Pro Pro Leu Gln Ala Leu Ala Arg Gly Gly Asn  
 405 410 415  
 Trp Leu Leu Val Pro Pro Leu Ser Leu Pro Ser Val  
 420 425

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTGGTCCTCC TTTGCAGAGG TGGTGCGGAG CTCCTGTTTG ACGGTATTAA GAAACATCGA 60  
 GTCACCTTTGC CTGGACAGGA GGAACCCTGG GACATCCGGA ACCTGCTCAT CTGGATCAAG 120  
 AAGAATTTGC TAAAAGAGCG GCCAGAGTTG TTCATCCAGG GAGACAGCGT GCGGCCAGGA 180  
 ATTCTGGTGC TGATTAACGA TGCCGACTGG GAGCTACTGG GTGAGCTGGA CTACCAGCTT 240  
 CAGGACCAGG ACAGCGTCCT CTTTCATCTCC ACTCTGCACG GCGGCTGAGG GCCCTTCTCT 300  
 GGGCCTGGGC ACCCTTAGAG GGGAGAACGA AGCAATCAGA CATCCCCTTG GGCCCTGCTT 360  
 CCAGGTCTCC CTGTCCCCCT TGCCTGCCTT CTTCCCTGCT CTGTCCCCTA AGCTCCCTCC 420  
 AGGCAGGGAA AAGAGGCCAG GTGCTAAAAA TGAGCCTTTC TCAAGCACGT GAGCAGCGGA 480  
 AGGCAGACAG GCGCCAGAGC CCAGCACTCC CTTTTCCAGC AGCTGTGGTG GGGGAGGGTT 540  
 CCCCTCCAGT TTGTCAAGAG TTGAAGGAGG CTCTGTGGCC AGGTGACCTG GCTGCCTTCC 600  
 ACTCCTTGTA CCTCAGTCTA AACATGGAGT GGCCGCTGAC AAGGCGCTCC AGCCCCAGAG 660  
 CCAGCGTCTT CATGGGGAAG ATGAATGGAC CTGAGTAGCT GAAGGAAGGC CCCTCCCTAC 720  
 CCAAAGACTG GAGGCTTCTC AGCCTCAATT TCCCTGTCTG TACAGCTGAG GGCTCTGCCT 780  
 GTCCCCCACT GCTATCAGTA TGGAACCCCA GCTGGGGTCC CCTATTGAGT GCCGACTCCC 840  
 CCCACCGCCA GCAGCTGCTC CTCCAGCCAC ACCCTTCCTG CTCCCCCCAC CCYTAGCCCT 900  
 TGACCCTGGC TGGCCTGCCC CGCTCCACAG GCCACCAGAT GGGCTCCTGA GACCCTCCCC 960  
 AGGCTGCTTA CAGCTCATTC TGCTGGGGGT AGAGATGAGG GGAGGGAGTA AGTTAAACCT 1020  
 TGGACTAGCA AGTAGAAGCC TGGGGGGATG CGTGTGCCTC AGTTTCCTC TCCACAACCTG 1080  
 AATATAGTGG CTGAAAACTG GGGAGATACT TGATGGCGCG AATGTCCGTT TTCTCTCCCT 1140

TCCCACCTCC TGCAGGAAGC AGGACGGGGC AGGCAGCACC TGGTAGGCAC AGTGCTTTGC 1200  
 CCCTCCTCCC CTTCCCTTCT GGAAGTCTTG GGGCCTCAGT GCTTGCAACA GCCGGCCTTG 1260  
 GGCAAATAAA AGACTAGGTT GTTTACTAAA AAAAAAAAAA AAAAAAAAAA 1309

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Ala Arg Met Ser Val Phe Ser Pro Phe Pro Pro Pro Ala Gly Ser  
 1 5 10 15  
 Arg Thr Gly Gln Ala Ala Pro Gly Arg His Ser Ala Leu Pro Leu Leu  
 20 25 30  
 Pro Phe Pro Ser Gly Ser Leu Gly Ala Ser Val Leu Ala Thr Ala Gly  
 35 40 45  
 Leu Gly Gln Ile Lys Asp  
 50

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1740 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGCCCGTGCG CTCCATCAAC CACGCCAGCC TCATCTCTGC ACTCTCCCGG GACTATCGCA 60  
 ACCTGAAGCC CAGTGCTGTT GCCCACAGA GAAAGATGCC ACTGGATGAC ACCAAACTGA 120  
 TTATCCACCA GAACTCAGC GTCTTAGAAG ATATTGTGGA GAATATCTCG GGGGAGTCCA 180  
 CCAAGTCTCG ACAGATTTGC TACCAGTCGC TGCAGGAATC TGTTCAAGTC TCCCTGGCCC 240  
 TCTTTCCAGC TTTTATCCAT CAGTCAGATG TGAATGATGA GATGCTGAGC TTCTTCCTCA 300  
 CTCTGTTTTG AGGCCTTAGA GTACAGATGG GTGTGCCTTT CACTGAGCAA ATCATAACAGA 360  
 CTTTCCTCAA CATGTTTACC AGAGAGCAGT TAGCCGAGAG CATCCTCCAC GAGGGCAGCA 420  
 CAGGCTGCCG GGTGGTGGAG AAGTTTCTGA AGATCCTGCA GGTGGTGGTC CAGGAGCCAG 480  
 GCCAGGTGTT CAAGCCCTTC CTCCCAGCA TCATCGCCCT GTGCATGGAG CAAGTGTATC 540

|                                                                   |      |
|-------------------------------------------------------------------|------|
| CCATCATTGC CGAGCGTCCC TCCCCTGATG TGAAGGCCGA GCTGTTTGAG CTCCTTTTCC | 600  |
| GGACGCTCCA TCACAAGTGG AGGTACTTCT TCAAGTCCAC CGTGCTGGCC AGTGTCAGAG | 660  |
| GGGGGATCGC TGAGGAGCAG ATGGAGAATG AGCCCCAGTT CAGTGCCATC ATGCAGGCTT | 720  |
| TCGGACAGTC CTTTCTCCAG CCCGACATCC ACCTTTTTTAA ACAAATCTC TTCTACTTGG | 780  |
| AGACTCTCAA CACCAAGCAG AAGCTGTACC ACAAGAAGAT CTTCCGGACT GCCATGCTGT | 840  |
| TCCAGTTTGT GAACGTGCTG CTCCAGGTCC TGGTCCACAA GTCCCATGAT CTTCTGCAGG | 900  |
| AGGAGATTGG CATCGCCATC TACAACATGG CCTCAGTCGA CTTTGATGGC TTCTTTGCCG | 960  |
| CCTTCCTCCC AGAGTTCCTG ACCAGCTGTG ATGGTGTGGA TGCCAACCAG AAAAGTGTGC | 1020 |
| TGGGGCGGAA TTTCAAGATG GATCGGGACC TGCCCTCATT CACCCAGAAT GTGCACAGGC | 1080 |
| TGGTCAACGA CCTGCGCTAC TACAGACTCT GCAACGACAG CCTGCCCCCT GGCAGTGTGA | 1140 |
| AGCTCTAGGC CTGCTACTGC CTGGGGACAC GGAATTCTGC TGCTGCCACC TGCGCCAGCC | 1200 |
| CTACCTTCCA CCACAGATGT CTCCCAGATG GGCCTTGGTC AACTCCTTG GCTTCTCCCA  | 1260 |
| CCGCAAGCAA CGCTGCCTGC CTCTGCCGCT CCTCCACATC TTGCCGCTGC CCAGCAGAGC | 1320 |
| TGGCTTCTGG GTCCACCTGA GCACTGGACG GTGCTCCCAG GGCGTTGGAG CAGGCGGAGG | 1380 |
| GGTGTGTGGC CAGGTACTAG GAGGCACCAG GAAATCCCGC GGGGTGGCCC ATGCAGACCA | 1440 |
| GGCGCACGTG GTCATGGGG CAGAATTGCC AAGGACAGCT CACGACAGTG CMACTTCTC   | 1500 |
| ACCATTCCAG CCAAGGAGAG ATGTGACGTT GGAAMTGYTY TGGCAMTTYT GTCAAGCCTC | 1560 |
| CCCCGCCCCA ATTGCCTTGA RATYTYTGCT CTTTGTGAGA GATTTGCAA GACTCAMGTT  | 1620 |
| TTTGTGTTT TCTCATCATT CCATTGTGAT ACTAAGAAAC TAAGAAGCTT AATGAAAAGA  | 1680 |
| AATAAAATGC CTATGTTGTT GTTCTAGGRR AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 1740 |

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 350 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Leu | Asp | Asp | Thr | Lys | Leu | Ile | Ile | His | Gln | Thr | Leu | Ser | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Glu | Asp | Ile | Val | Glu | Asn | Ile | Ser | Gly | Glu | Ser | Thr | Lys | Ser | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Ile | Cys | Tyr | Gln | Ser | Leu | Gln | Glu | Ser | Val | Gln | Val | Ser | Leu | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Leu Phe Pro Ala Phe Ile His Gln Ser Asp Val Thr Asp Glu Met Leu  
 50 55 60  
 Ser Phe Phe Leu Thr Leu Phe Arg Gly Leu Arg Val Gln Met Gly Val  
 65 70 75 80  
 Pro Phe Thr Glu Gln Ile Ile Gln Thr Phe Leu Asn Met Phe Thr Arg  
 85 90 95  
 Glu Gln Leu Ala Glu Ser Ile Leu His Glu Gly Ser Thr Gly Cys Arg  
 100 105 110  
 Val Val Glu Lys Phe Leu Lys Ile Leu Gln Val Val Val Gln Glu Pro  
 115 120 125  
 Gly Gln Val Phe Lys Pro Phe Leu Pro Ser Ile Ile Ala Leu Cys Met  
 130 135 140  
 Glu Gln Val Tyr Pro Ile Ile Ala Glu Arg Pro Ser Pro Asp Val Lys  
 145 150 155 160  
 Ala Glu Leu Phe Glu Leu Leu Phe Arg Thr Leu His His Asn Trp Arg  
 165 170 175  
 Tyr Phe Phe Lys Ser Thr Val Leu Ala Ser Val Gln Arg Gly Ile Ala  
 180 185 190  
 Glu Glu Gln Met Glu Asn Glu Pro Gln Phe Ser Ala Ile Met Gln Ala  
 195 200 205  
 Phe Gly Gln Ser Phe Leu Gln Pro Asp Ile His Leu Phe Lys Gln Asn  
 210 215 220  
 Leu Phe Tyr Leu Glu Thr Leu Asn Thr Lys Gln Lys Leu Tyr His Lys  
 225 230 235 240  
 Lys Ile Phe Arg Thr Ala Met Leu Phe Gln Phe Val Asn Val Leu Leu  
 245 250 255  
 Gln Val Leu Val His Lys Ser His Asp Leu Leu Gln Glu Glu Ile Gly  
 260 265 270  
 Ile Ala Ile Tyr Asn Met Ala Ser Val Asp Phe Asp Gly Phe Phe Ala  
 275 280 285  
 Ala Phe Leu Pro Glu Phe Leu Thr Ser Cys Asp Gly Val Asp Ala Asn  
 290 295 300  
 Gln Lys Ser Val Leu Gly Arg Asn Phe Lys Met Asp Arg Asp Leu Pro  
 305 310 315 320  
 Ser Phe Thr Gln Asn Val His Arg Leu Val Asn Asp Leu Arg Tyr Tyr  
 325 330 335  
 Arg Leu Cys Asn Asp Ser Leu Pro Pro Gly Thr Val Lys Leu  
 340 345 350

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ANTGTCTTGA CTACAAGCTC CACGGGGGC

29

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TNGCCAAGGA GAAAGCGAGG CAGACAAGG

29

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ANATCGACTC TTTGCATCGC ACATTTTGT

29

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CNTTCTTCGG ACTTATGTTT GAATCTATC

29

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CNTTCCTCTT AGATCTCAGT ATCCACCTC

29

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CNCAGACAGG GGAGATAACA ATGAGGTGC

29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TNCTATAGGT GACTTCACCC TGTCAGGAG

29

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TNTTACAGGA GCAGGACGCG AGCAGAGAG

29

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ANTCAGTTGT GGAGGAGGAA ACTGAGGCA

29

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CNTCGAAACA GAGTGAGGAA GAAGCTCAG

29

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ala | Trp | Arg | Ser | Ala | Phe | Leu | Val | Cys | Leu | Ala | Phe | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Thr | Leu | Val | Gln | Arg | Gly | Ser | Gly | Asp | Phe | Asp | Asp | Phe | Asn | Leu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asp | Ala | Val | Lys | Glu | Thr | Ser | Ser | Val | Lys | Gln | Pro | Trp | Asp | His |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Thr | Thr | Thr | Thr | Thr | Asn | Arg | Pro | Gly | Thr | Thr | Arg | Ala | Pro | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Pro | Pro | Gly | Ser | Gly | Leu | Asp | Leu | Ala | Asp | Ala | Leu | Asp | Asp | Gln |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Asp | Gly | Arg | Arg | Lys | Pro | Gly | Ile | Gly | Gly | Arg | Glu | Arg | Trp | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Val | Thr | Thr | Thr | Thr | Lys | Arg | Pro | Val | Thr | Thr | Arg | Ala | Pro | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Thr | Leu | Gly | Asn | Asp | Phe | Asp | Leu | Ala | Asp | Ala | Leu | Asp | Asp | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Asp | Arg | Asp | Asp | Gly | Arg | Arg | Lys | Pro | Ile | Ala | Gly | Gly | Gly | Gly |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|



|                                                                 |     |             |
|-----------------------------------------------------------------|-----|-------------|
| 130                                                             | 135 | 140         |
| Phe Ser Asp Lys Asp Leu Glu Asp Ile Val Gly Gly Gly Glu Tyr Lys |     |             |
| 145                                                             | 150 | 155 160     |
| Pro Asp Lys Gly Lys Gly Asp Gly Arg Tyr Gly Ser Asn Asp Asp Pro |     |             |
|                                                                 | 165 | 170 175     |
| Gly Ser Gly Met Val Ala Glu Pro Gly Thr Ile Ala Gly Val Ala Ser |     |             |
|                                                                 | 180 | 185 190     |
| Ala Leu Ala Met Ala Leu Ile Gly Ala Val Ser Ser Tyr Ile Ser Tyr |     |             |
|                                                                 | 195 | 200 205     |
| Gln Gln Lys Lys Phe Cys Phe Ser Ile Gln Gln Gly Leu Asn Ala Asp |     |             |
|                                                                 | 210 | 215 220     |
| Tyr Val Lys Gly Glu Asn Leu Glu Ala Val Val Cys Glu Glu Pro Gln |     |             |
|                                                                 | 225 | 230 235 240 |
| Val Lys Tyr Ser Thr Leu His Thr Gln Ser Ala Glu Pro Pro Pro Pro |     |             |
|                                                                 | 245 | 250 255     |
| Pro Glu Pro Ala Arg Ile                                         |     |             |
|                                                                 | 260 |             |

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

|                                                                 |     |          |
|-----------------------------------------------------------------|-----|----------|
| Met His Val Leu Glu Thr Leu Asp Leu Leu Val Leu Arg Ala Asp Lys |     |          |
| 1                                                               | 5   | 10 15    |
| Gly Lys Asp Ala Arg Leu Phe Val Phe Arg Leu Ser Ala Leu Gln Lys |     |          |
|                                                                 | 20  | 25 30    |
| Gly Leu Glu Gly Lys Gln Ala Gly Lys Ser Arg Ser Asp Cys Arg Glu |     |          |
|                                                                 | 35  | 40 45    |
| Asn Lys Leu Glu Lys Thr Lys Gly Cys His Leu Tyr Ala Ile Asn Thr |     |          |
|                                                                 | 50  | 55 60    |
| His His Ser Arg Glu Leu Arg Ile Val Val Ala Ile Arg Asn Lys Leu |     |          |
|                                                                 | 65  | 70 75 80 |
| Leu Leu Ile Thr Arg Lys His Asn Lys Pro Ser Gly Val Thr Ser Thr |     |          |
|                                                                 | 85  | 90 95    |
| Ser Leu Leu Ser Pro Leu Ser Glu Ser Pro Val Glu Glu Phe Gln Tyr |     |          |
|                                                                 | 100 | 105 110  |
| Ile Arg Glu Ile Cys Leu Ser Asp Ser Pro Met Val Met Thr Leu Val |     |          |
|                                                                 | 115 | 120 125  |

Asp Gly Pro Ala Glu Glu Ser Asp Asn Leu Ile Cys Val Ala Tyr Arg  
 130 135 140  
 His Gln Phe Asp Val Val Asn Glu Ser Thr Gly Glu Ala Phe Arg Leu  
 145 150 155 160  
 His His Val Glu Ala Asn Arg Val Asn Phe Val Ala Ala Ile Asp Val  
 165 170 175  
 Tyr Glu Asp Gly Glu Ala Gly Leu Leu Leu Cys Tyr Asn Tyr Ser Cys  
 180 185 190  
 Ile Tyr Lys Lys Val Cys Pro Phe Asn Gly Gly Ser Phe Leu Val Gln  
 195 200 205  
 Pro Ser Ala Ser Asp Phe Gln Phe Cys Trp Asn Gln Ala Pro Tyr Ala  
 210 215 220  
 Ile Val Cys Ala Phe Pro Tyr Leu Leu Ala Phe Thr Thr Asp Ser Met  
 225 230 235 240  
 Glu Ile Arg Leu Val Val Asn Gly Asn Leu Val His Thr Ala Val Val  
 245 250 255  
 Pro Gln Leu Gln Leu Val Ala Ser Arg Ser Asp Ile Tyr Phe Thr Ala  
 260 265 270  
 Thr Ala Ala Val Asn Glu Val Ser Ser Gly Gly Ser Ser Lys Gly Ala  
 275 280 285  
 Ser Ala Arg Asn Ser Pro Gln Thr Pro Pro Gly Arg Asp Thr Pro Val  
 290 295 300  
 Phe Pro Ser Ser Leu Gly Glu Gly Glu Ile Gln Ser Lys Asn Leu Tyr  
 305 310 315 320  
 Lys Ile Pro Leu Arg Asn Leu Val Gly Arg Ser Ile Glu Arg Pro Leu  
 325 330 335  
 Lys Ser Pro Leu Val Ser Lys Val Ile Thr Pro Pro Thr Pro Ile Ser  
 340 345 350  
 Val Gly Leu Ala Ala Ile Pro Val Thr His Ser Leu Ser Leu Ser Arg  
 355 360 365  
 Met Glu Ile Lys Glu Ile Ala Ser Arg Thr Arg Arg Glu Leu Leu Gly  
 370 375 380  
 Leu Ser Asp Glu Gly Gly Pro Lys Ser Glu Gly Ala Pro Lys Ala Lys  
 385 390 395 400  
 Ser Lys Pro Arg Lys Arg Leu Glu Glu Ser Gln Gly Gly Pro Lys Pro  
 405 410 415  
 Gly Ala Val Arg Ser Ser Ser Ser Asp Arg Ile Pro Ser Gly Ser Leu  
 420 425 430  
 Glu Ser Ala Ser Thr Ser Glu Ala Asn Pro Glu Gly His Ser Ala Ser  
 435 440 445

Ser Asp Gln Asp Pro Val Ala Asp Arg Glu Gly Ser Pro Val Ser Gly  
450 455 460

Ser Ser Pro Phe Gln Leu Thr Ala Phe Ser Asp Glu Asp Ile Ile Asp  
465 470 475 480

Leu Lys

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GTTTAGTGAT ACGACACAAG ATCGGGAGAT TTTTGATCAC CATACTGAAG AGGATATAGA  | 60   |
| TAAAAGTGCT AACAGTGTAT TGATAAAAAA CCTGAGCAGG ACCCCATCTA GTTGCAGCAG  | 120  |
| CTCTCTGGAT TCAATCAAGG CTGATGGGAC CTCTCTGGAC TTCAGCACTT ACCGCAGTAG  | 180  |
| TCAAATGGAA TCACAGTTTC TCAGAGATAC TATTTGTGAA GAGAGCTTGA GGGAGAAACT  | 240  |
| CCAAGATGGG AGAATAACAA TAAGGGAGTT CTTTATACTT CTCCAGGTCC ACATCTTGAT  | 300  |
| ACAGAAACCC CGACAGAGCA ATCTCCCAGG CAATTTTACT GTAAACACAC CACCTACTCC  | 360  |
| AGAAGACCTG ATGTTAAGTC AATATGTTTA CCGACCCAAG ATACAGATTT ATAGAGAAGA  | 420  |
| TTGTGAGGCT CGTCGCCAAA AGATTGAAGA ATTAAAGCTT TCTGCATCGA ACCAAGATAA  | 480  |
| GCTGTTGGTT GATATAAATA AGAACCTGTG GGAAAAAATG AGACACTGCT CTGACAAAAGA | 540  |
| GCTGAAGGCC TTTGGAATTT ATCTTAACAA AATAAAGTCA TGTTTTACCA AGATGACTAA  | 600  |
| AGTCTTCACT CACCAAGGAA AAGTGGCTCT GTATGGCAAG CTGGTGCAGT CAGCTCAGAA  | 660  |
| TGAGAGGGAG AAACTTCAAA TAAAGATAGA TGAGATGGAT AAAATACTTA AGAAGATCGA  | 720  |
| TAACTGCCTC ACTGAGATGG AAACAGAAAC TAAGAATTTG GAGGATGAAG AGAAAAACAA  | 780  |
| TCCTGTGGAA GAATGGGATT CTGAAATGAG AGCTGCAGAA AAAGAATTGG AACAGCTGAA  | 840  |
| AACTGAAGAG GAGGAGCTTC AAAGAAATCT CTTAGAACTG GAGGTACCAA AAGAGCAGAC  | 900  |
| CCTTGCTCAA ATAGACTTTA TGCAAAAACA AAGAAATAGA ACTGAAGAGC TACTGGATCA  | 960  |
| GTTGAGCTTG TCTGAGTGGG ATGTCGTTGA GTGGAGTGAT GATCAAGCTG TATTCACCTT  | 1020 |
| TGTTTATGAC ACGATACAAC TCACCATCAC CTTTGAAGAG TCAGTTGTTG GTTTCCTTTT  | 1080 |
| CCTGGACAAG CGTTATAGGA AGATTGTTGA TGTCATTTT CAATCTCTGT TAGATGAGGA   | 1140 |
| TCAAGCTCCT CCTTCCTCCC TTTTAGTTCA TAAGCTTATT TTCCAGTACG TTGAAGAAAA  | 1200 |
| GGAATCCTGG AAGAAGACAT GTACAACCCA GCATCAGTTA CCCAAGATGC TTGAAGAATT  | 1260 |

CTCACTGGTA GTGCACCATT GCAGACTCCT TGGAGAGGAG ATTGAGTATT TAAAGAGATG 1320  
 GGGACCAAAT TATAACCTAA TGAACATAGA TATTAATAAT AATGAATTGA GACTTTTATT 1380  
 CTCTAGCTCC GCAGCATTTG CAAAGTTTGA AATAACTTTG TTTCTCTCAG CCTATTATCC 1440  
 ATCTGTACCA TTACCTTCCA CCATTTCAGAA TCACGTTGGG AACACTAGCC AAGATGATAT 1500  
 TGCTACCATT CTATCTAAAG TGCCACTGGA GAACAACTAC CTGAAGAATG TAGTCAAGCA 1560  
 AATTTACCAA GATCTGTTTC AGGACTGCCA TTTCTACCAC TAGACCCTTG GACCACCATT 1620  
 GGAACAACCA AGCAGAATGT ACTTGATATT ATTCAGGGT CCCATTGCTG TTCAGCCTTT 1680  
 GTTTTTACGT CATTACAAGC TGAGTAAAAT TCCTTCTGAT GATGTTATAA AAAAAAAAAA 1740  
 AAAAAAAAAA 1748

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ser | Gln | Phe | Leu | Arg | Asp | Thr | Ile | Cys | Glu | Glu | Ser | Leu | Arg | 1   | 5   | 10  | 15  |
| Glu | Lys | Leu | Gln | Asp | Gly | Arg | Ile | Thr | Ile | Arg | Glu | Phe | Phe | Ile | Leu | 20  | 25  | 30  |     |
| Leu | Gln | Val | His | Ile | Leu | Ile | Gln | Lys | Pro | Arg | Gln | Ser | Asn | Leu | Pro | 35  | 40  | 45  |     |
| Gly | Asn | Phe | Thr | Val | Asn | Thr | Pro | Pro | Thr | Pro | Glu | Asp | Leu | Met | Leu | 50  | 55  | 60  |     |
| Ser | Gln | Tyr | Val | Tyr | Arg | Pro | Lys | Ile | Gln | Ile | Tyr | Arg | Glu | Asp | Cys | 65  | 70  | 75  | 80  |
| Glu | Ala | Arg | Arg | Gln | Lys | Ile | Glu | Glu | Leu | Lys | Leu | Ser | Ala | Ser | Asn | 85  | 90  | 95  |     |
| Gln | Asp | Lys | Leu | Leu | Val | Asp | Ile | Asn | Lys | Asn | Leu | Trp | Glu | Lys | Met | 100 | 105 | 110 |     |
| Arg | His | Cys | Ser | Asp | Lys | Glu | Leu | Lys | Ala | Phe | Gly | Ile | Tyr | Leu | Asn | 115 | 120 | 125 |     |
| Lys | Ile | Lys | Ser | Cys | Phe | Thr | Lys | Met | Thr | Lys | Val | Phe | Thr | His | Gln | 130 | 135 | 140 |     |
| Gly | Lys | Val | Ala | Leu | Tyr | Gly | Lys | Leu | Val | Gln | Ser | Ala | Gln | Asn | Glu | 145 | 150 | 155 | 160 |

Arg Glu Lys Leu Gln Ile Lys Ile Asp Glu Met Asp Lys Ile Leu Lys  
165 170 175

Lys Ile Asp Asn Cys Leu Thr Glu Met Glu Thr Glu Thr Lys Asn Leu  
180 185 190

Glu Asp Glu Glu Lys Asn Asn Pro Val Glu Glu Trp Asp Ser Glu Met  
195 200 205

Arg Ala Ala Glu Lys Glu Leu Glu Gln Leu Lys Thr Glu Glu Glu Glu  
210 215 220

Leu Gln Arg Asn Leu Leu Glu Leu Glu Val Pro Lys Glu Gln Thr Leu  
225 230 235 240

Ala Gln Ile Asp Phe Met Gln Lys Gln Arg Asn Arg Thr Glu Glu Leu  
245 250 255

Leu Asp Gln Leu Ser Leu Ser Glu Trp Asp Val Val Glu Trp Ser Asp  
260 265 270

Asp Gln Ala Val Phe Thr Phe Val Tyr Asp Thr Ile Gln Leu Thr Ile  
275 280 285

Thr Phe Glu Glu Ser Val Val Gly Phe Pro Phe Leu Asp Lys Arg Tyr  
290 295 300

Arg Lys Ile Val Asp Val Asn Phe Gln Ser Leu Leu Asp Glu Asp Gln  
305 310 315 320

Ala Pro Pro Ser Ser Leu Leu Val His Lys Leu Ile Phe Gln Tyr Val  
325 330 335

Glu Glu Lys Glu Ser Trp Lys Lys Thr Cys Thr Thr Gln His Gln Leu  
340 345 350

Pro Lys Met Leu Glu Glu Phe Ser Leu Val Val His His Cys Arg Leu  
355 360 365

Leu Gly Glu Glu Ile Glu Tyr Leu Lys Arg Trp Gly Pro Asn Tyr Asn  
370 375 380

Leu Met Asn Ile Asp Ile Asn Asn Asn Glu Leu Arg Leu Leu Phe Ser  
385 390 395 400

Ser Ser Ala Ala Phe Ala Lys Phe Glu Ile Thr Leu Phe Leu Ser Ala  
405 410 415

Tyr Tyr Pro Ser Val Pro Leu Pro Ser Thr Ile Gln Asn His Val Gly  
420 425 430

Asn Thr Ser Gln Asp Asp Ile Ala Thr Ile Leu Ser Lys Val Pro Leu  
435 440 445

Glu Asn Asn Tyr Leu Lys Asn Val Val Lys Gln Ile Tyr Gln Asp Leu  
450 455 460

Phe Gln Asp Cys His Phe Tyr His  
465 470

(2) INFORMATION FOR SEQ ID NO:69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| CTTTTCTTTG ATTGTCTCTG CTTTAGCGTC TCTAAATCCG GTCACCATGT CGGACCCCGA  | 60   |
| AGGCGAGACC TTGCGAAGCA CCTTTCCTC TTATATGGCC GAAGGCGAGC GGCTCTACCT   | 120  |
| GTGCGGGGAA TTTTCTAAAG CCGCGCAGAG CTTCAGCAAC GCTCTTTACC TTCAGGATGG  | 180  |
| AGACAAGAAC TGCCTGGTTG CTCGCTCAAA GTGCTTCCTG AAGATGGGAG ACTTGAGAG   | 240  |
| ATCCCTGAAG GATGCTGARG CTTGCTCCA GAGTGACCCA GCTTTCTGTA AGGGGATTTT   | 300  |
| GCAAAGGCT GAGACACTGT ACACCATGGG AGACTTTGAG TTTGCCTTGG TATTCTATCA   | 360  |
| TCGARGCTAC AAGCTGARGC CTGATCGGGA ATTCARARTT GGCATTGAGA AAGCCCAGGA  | 420  |
| AGCCATCAAC AACTCAGTGG GAAGTCCTC TTCCATTAAG CTGGAGAACA AAGGGGACCT   | 480  |
| CTCCTTCTTA AGCAAGCAGG CTGAGAATAT AAAAGCCCAG CAGAAGCCTC AGCCCATGAA  | 540  |
| ACACCTCTTA CACCCACCA AGGGAGAGCC CAAGTGGAAG GCCTCGCTCA AGAGTGAGAA   | 600  |
| GACTGTCCGC CAGCTTCTGG GGGAGCTCTA CGTGGACAAA GAGTATTTGG AGAAGCTCCT  | 660  |
| ATTGGATGAA GACCTGATCA AAGGCACCAT GAAGGGCGGC CTGACTGTGG AGGACCTCAT  | 720  |
| CATGACGGGC ATCAACTACC TGGATACTCA CAGCAACTTC TGGAGGCAGC AGAAGCCGAT  | 780  |
| CTACGCCAGG GAGCGGGACC GGAAGCTGAT GCAAGAGAAA TGGCTGCGGG ACCACAAACG  | 840  |
| CCGTCCCTCA CAGACAGCCC ATTACATCCT CAAGAGCCTG GAGGACATTG ATATGTTGCT  | 900  |
| CACAAGTGGC AGTGCTGAAG GGAGTCTTCA GAAAGCTGAG AAAGTGCTGA AGAAGGTACT  | 960  |
| GGAATGGAAC AAGGAAGAGG TACCCAACAA GGATGAACTG GTTGGAAGT TGTATAGCTG   | 1020 |
| CATAGGGAAT GCCCAGATTG AGCTGGGGCA GATGGAGGCA GCCCTGCAGA GCCACAGAAA  | 1080 |
| GGACYTGGAG ATCGCCAAGG AATATGACCT TCCTGATGCA AAATCGAGAG CCCTTGACAA  | 1140 |
| CATTGGCAGA GTTTTTGCCA GAGTTGGGAA ATTCCAGCAA GCCATTGACA CGTGGGAAGA  | 1200 |
| AAAGATCCCT CTGGCAAAAA CCACCCTGGA GAAGACCTGG CTGTTCCACG AGATCGGGCCG | 1260 |
| CTGCTACTTG GAGCTGGACC AGGCCTGGCA GGCCAGAAT TATGGCGAGA AGTCCCAGCA   | 1320 |
| GTGTGCCGAG GAGGAAGGGG ACATTGAGTG GCAACTGAAT GCCAGTGTTT TGGTGGCCCA  | 1380 |
| GGCACAAGTG AAGCTGAGAG ACTTCGAGTC AGCCGTGAAC AATTTTGAGA AGGCCCTGGA  | 1440 |
| GAGAGCAAAG CTTGTGCATA ACAACGAGGC GCAGCAGGCC ATCATCAGTG CCTTGACGA   | 1500 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| TGCCAACAAG GGTATCATCA GAGAACTGAG GAAAACCAAC TACGTGGAGA ATCTCAAAGA | 1560 |
| AAAAAGCGAG GGAGAAGCTT CACTGTATGA AGATAGAATA ATAACAAGAG AGAAGGACAT | 1620 |
| GAGGAGAGTG AGAGATGAGC CCGAGAAGGT GGTGAAGCAG TGGGACCATA GTGAGGATGA | 1680 |
| GAAAGAGACA GATGAGGACG ATGAGGCTTT TGGGGAAGCT CTGCAGAGCC CAGCAAGCGG | 1740 |
| AAAGCAGAGT GTGGAAGCAG GAAAAGCCAG AAGCGATTG GGAGCAGTTG CCAAGGGCCT  | 1800 |
| GTCAGGAGAA TTAGGCACAA GATCAGGAGA AACAGGCAGG AAGCTACTAG AAGCTGGCAG | 1860 |
| AAGAGAGTCA AGAGAAATTT ATAGGAGGCC TTCGGGAGAA TTAGAGCAAA GACTCTCAGG | 1920 |
| AGAATTCAGC AGACAGGAAC CAGAAGAACT AAAGAACTT TCAGAAGTGG GCAGAAGAGA  | 1980 |
| SCCAGAAGAA YTGGGAAAAA CACAATTTGG AGAAATAGGA GAAACGAAAA AAACAGGAAA | 2040 |
| TGAGATGGAA AAGGAATATG AATGAAGCCA TCGGTAGAGA TGAGGATCAG GAAGCTGGTG | 2100 |
| TTCAGAGGGA TCATGGGATT TTATTAACT GGATTTTCAA GCGATTTGTC TGTTATAGGA  | 2160 |
| AAAATGAGGG TTTTACTTYT GCTGCTTTCC ATCACTATTT TGCCATTAAA TAGGTGTCTT | 2220 |
| TCACTCTTGC MAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 2280 |
| AAAAAAAAAA AAAAAAAAAA                                             | 2298 |

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ser Asp Pro Glu Gly Glu Thr Leu Arg Ser Thr Phe Pro Ser Tyr |  |
| 1 5 10 15                                                       |  |
| Met Ala Glu Gly Glu Arg Leu Tyr Leu Cys Gly Glu Phe Ser Lys Ala |  |
| 20 25 30                                                        |  |
| Ala Gln Ser Phe Ser Asn Ala Leu Tyr Leu Gln Asp Gly Asp Lys Asn |  |
| 35 40 45                                                        |  |
| Cys Leu Val Ala Arg Ser Lys Cys Phe Leu Lys Met Gly Asp Leu Glu |  |
| 50 55 60                                                        |  |
| Arg Ser Leu Lys Asp Ala Glu Ala Ser Leu Gln Ser Asp Pro Ala Phe |  |
| 65 70 75 80                                                     |  |
| Cys Lys Gly Ile Leu Gln Lys Ala Glu Thr Leu Tyr Thr Met Gly Asp |  |
| 85 90 95                                                        |  |
| Phe Glu Phe Ala Leu Val Phe Tyr His Arg Xaa Tyr Lys Leu Xaa Pro |  |
| 100 105 110                                                     |  |

Asp Arg Glu Phe Xaa Xaa Gly Ile Gln Lys Ala Gln Glu Ala Ile Asn  
 115 120 125  
 Asn Ser Val Gly Ser Pro Ser Ser Ile Lys Leu Glu Asn Lys Gly Asp  
 130 135 140  
 Leu Ser Phe Leu Ser Lys Gln Ala Glu Asn Ile Lys Ala Gln Gln Lys  
 145 150 155 160  
 Pro Gln Pro Met Lys His Leu Leu His Pro Thr Lys Gly Glu Pro Lys  
 165 170 175  
 Trp Lys Ala Ser Leu Lys Ser Glu Lys Thr Val Arg Gln Leu Leu Gly  
 180 185 190  
 Glu Leu Tyr Val Asp Lys Glu Tyr Leu Glu Lys Leu Leu Leu Asp Glu  
 195 200 205  
 Asp Leu Ile Lys Gly Thr Met Lys Gly Gly Leu Thr Val Glu Asp Leu  
 210 215 220  
 Ile Met Thr Gly Ile Asn Tyr Leu Asp Thr His Ser Asn Phe Trp Arg  
 225 230 235 240  
 Gln Gln Lys Pro Ile Tyr Ala Arg Glu Arg Asp Arg Lys Leu Met Gln  
 245 250 255  
 Glu Lys Trp Leu Arg Asp His Lys Arg Arg Pro Ser Gln Thr Ala His  
 260 265 270  
 Tyr Ile Leu Lys Ser Leu Glu Asp Ile Asp Met Leu Leu Thr Ser Gly  
 275 280 285  
 Ser Ala Glu Gly Ser Leu Gln Lys Ala Glu Lys Val Leu Lys Lys Val  
 290 295 300  
 Leu Glu Trp Asn Lys Glu Glu Val Pro Asn Lys Asp Glu Leu Val Gly  
 305 310 315 320  
 Asn Leu Tyr Ser Cys Ile Gly Asn Ala Gln Ile Glu Leu Gly Gln Met  
 325 330 335  
 Glu Ala Ala Leu Gln Ser His Arg Lys Asp Leu Glu Ile Ala Lys Glu  
 340 345 350  
 Tyr Asp Leu Pro Asp Ala Lys Ser Arg Ala Leu Asp Asn Ile Gly Arg  
 355 360 365  
 Val Phe Ala Arg Val Gly Lys Phe Gln Gln Ala Ile Asp Thr Trp Glu  
 370 375 380  
 Glu Lys Ile Pro Leu Ala Lys Thr Thr Leu Glu Lys Thr Trp Leu Phe  
 385 390 395 400  
 His Glu Ile Gly Arg Cys Tyr Leu Glu Leu Asp Gln Ala Trp Gln Ala  
 405 410 415  
 Gln Asn Tyr Gly Glu Lys Ser Gln Gln Cys Ala Glu Glu Glu Gly Asp  
 420 425 430  
 Ile Glu Trp Gln Leu Asn Ala Ser Val Leu Val Ala Gln Ala Gln Val



|                                                                                    |     |     |
|------------------------------------------------------------------------------------|-----|-----|
| 435                                                                                | 440 | 445 |
| Lys Leu Arg Asp Phe Glu Ser Ala Val Asn Asn Phe Glu Lys Ala Leu<br>450 455 460     |     |     |
| Glu Arg Ala Lys Leu Val His Asn Asn Glu Ala Gln Gln Ala Ile Ile<br>465 470 475 480 |     |     |
| Ser Ala Leu Asp Asp Ala Asn Lys Gly Ile Ile Arg Glu Leu Arg Lys<br>485 490 495     |     |     |
| Thr Asn Tyr Val Glu Asn Leu Lys Glu Lys Ser Glu Gly Glu Ala Ser<br>500 505 510     |     |     |
| Leu Tyr Glu Asp Arg Ile Ile Thr Arg Glu Lys Asp Met Arg Arg Val<br>515 520 525     |     |     |
| Arg Asp Glu Pro Glu Lys Val Val Lys Gln Trp Asp His Ser Glu Asp<br>530 535 540     |     |     |
| Glu Lys Glu Thr Asp Glu Asp Asp Glu Ala Phe Gly Glu Ala Leu Gln<br>545 550 555 560 |     |     |
| Ser Pro Ala Ser Gly Lys Gln Ser Val Glu Ala Gly Lys Ala Arg Ser<br>565 570 575     |     |     |
| Asp Leu Gly Ala Val Ala Lys Gly Leu Ser Gly Glu Leu Gly Thr Arg<br>580 585 590     |     |     |
| Ser Gly Glu Thr Gly Arg Lys Leu Leu Glu Ala Gly Arg Arg Glu Ser<br>595 600 605     |     |     |
| Arg Glu Ile Tyr Arg Arg Pro Ser Gly Glu Leu Glu Gln Arg Leu Ser<br>610 615 620     |     |     |
| Gly Glu Phe Ser Arg Gln Glu Pro Glu Glu Leu Lys Lys Leu Ser Glu<br>625 630 635 640 |     |     |
| Val Gly Arg Arg Xaa Pro Glu Glu Leu Gly Lys Thr Gln Phe Gly Glu<br>645 650 655     |     |     |
| Ile Gly Glu Thr Lys Lys Thr Gly Asn Glu Met Glu Lys Glu Tyr Glu<br>660 665 670     |     |     |

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGAAGAGCCA CCATCCCTGC CCCCCTTTTC CCACCGGGGA GTCTGTACAG AGATTTTCT  | 60  |
| ACGTTTTTAT TTTTGCCTC AGAGGGATGG GATTGGGGAG GAGGGGATGG GCAGCGGAGG  | 120 |
| GTTGGGGGCA TGGTCTGCAG GCTCATCTGT GTCCGCCTTT CACTCCACTA ATGCTGTCTC | 180 |

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AGTGT TTTCT CTCTCTCTCT TTCGAGCTTG CACTCCGGTA CCCGACCCGG CGCCCTGGCC 240
CATCCCATGC CGGGGGGCCA GTGGAAAGAA GACAGGCCGT CCAGCCCGTG CCCGCCTGCG 300
GCGGGGGCAC CCAGCAAGCC CGCCCACCGC CCGCTGCCTC ACCTGCTTCG CCACAGACTC 360
TTGTTCCCAG CCCCTTGGGG CCTCCGTGTT TGGGGTGGGG GAGCTGCTTA GAGACTGTGC 420
CCGTCCTCGG CCCCCACCC TGAAGTGCCA GCACCACCAG CACCAGATCT TCCGCCGCCA 480
CACCGCATTG AGGACACGCC GGCCGGGCCG CTTCGTCTCA AGTTGTATAA AGTTGTCTCC 540
GTGTCCCCTC CTCCCTCTGC CCCCAGTGTT TCTTCTGATT TTTTTTCCC CTTTCCCTCC 600
CTCCCTCTCC GCATTCTTCC CTTGGTTCAG CACAGGTAAA ACGGTTCCCC TCCCTCCCTG 660
CCTTCATGGA TCACCAGCTC ACGTCATGTT GCCTTCTCTT TTCTTTGTGT GTGTGTTTAT 720
TTAAGTTATT TTTCTTCCTC CTCTCCCTTT TCTTTTGGC CCTCCCTCCC TCCCTCTTCT 780
GCCATGTAAC TGGAGGATGT GCTATGAGTT TGCAAACAGC TGGACTGTCA GGCTGCTTTT 840
TTTTCCAGAT GTTCTTCTTC TGCTTCCCCT TCCCCTCCTC TCCCCTCCTT TTCCTTCCTT 900
CCTTCCTTTC CTTGGAGCAC TGAGCACCAT TTGGAAGCTT GAGAGAAACC AAAATTAAAG 960
AGAGAAAGAG AGAGCGTGCA CGCTCCTGCT TTGTCAAAAA AAAAAAAAAA 1010

```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

Met Gly Ser Gly Gly Leu Gly Ala Trp Ser Ala Gly Ser Ser Val Ser
1 5 10 15
Ala Phe His Ser Thr Asn Ala Val Ser Val Phe Ser Leu Ser Leu Phe
20 25 30
Arg Ala Cys Thr Pro Val Pro Asp Pro Ala Pro Trp Pro Ile Pro Cys
35 40 45
Arg Gly Ala Ser Gly Lys Lys Thr Gly Arg Pro Ala Arg Ala Arg Leu
50 55 60
Arg Arg Gly His Pro Ala Ser Pro Pro Thr Ala Arg Cys Leu Thr Cys
65 70 75 80
Phe Ala Thr Asp Ser Cys Ser Gln Pro Leu Gly Ala Ser Val Phe Gly
85 90 95
Val Gly Glu Leu Leu Arg Asp Cys Ala Arg Pro Arg Pro Pro Thr Leu
100 105 110

```

Lys Cys Gln His His Gln His Gln Ile Phe Arg Arg His Thr Ala Leu  
115 120 125  
Arg Thr Arg Arg Pro Gly Arg Phe Val Ser Ser Cys Ile Lys Leu Ser  
130 135 140  
Pro Cys Pro Leu Leu Pro Leu Pro Pro Val Phe Leu Leu Ile Phe Phe  
145 150 155 160  
Ser Pro Phe Pro Pro Ser Leu Ser Ala Phe Phe Pro Trp Phe Ser Thr  
165 170 175  
Gly Lys Thr Val Pro Leu Pro Pro Cys Leu His Gly Ser Pro Ala His  
180 185 190  
Val Met Leu Pro Ser Leu Phe Phe Val Cys Val Phe Ile  
195 200 205

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATTTYGCTCA TCAACCTCAT TATAGAACAT ATGATTTGTG ATACAGATCC TGAAGTTGGA 60  
GGAGCAGTCC AGCTTATGGG CCTGCTTCGA ACTTTAGTTG ACCCAGAGAA CATGCTAGCC 120  
ACTGCCMATA AAACASAAAA GACTGAATTT CTGGGTTTCT TCTACAAGCA CTGTATGCAT 180  
GTTCTCWCTG CTCCTTTACT AGCAAATACA ACAGAAGACA AACCTAGTAA AGATGATTTT 240  
CAGACTGCCC AACTATTGGC ACTTGTATTG GAATTGTTAA CATTTTGTGT GGAGCACCAT 300  
ACCTACCACA TAAAGAACTA CATTATTAAT AAGGATATCC TCCGGAGAGT GCTAGTTCTT 360  
ATGGCCTCGA AGCATGCTTT CTTGGCATTG TGTGCCCTTC GTTTTAAAAG AAAGATTATT 420  
GGATTAAAAG ATGAGTTTTA CAACCGCTAC ATAATGAAAA GTTTTTTGTT TGAACAGTA 480  
GTGAAAGCAT TTCTCAACAA TGGATCCCGC TACAATCTGA TGAAGTCTGC CATAATAGAG 540  
ATGTTTGAAT TTATTAGAGT GGAAGATATA AAATCATTA CTGCTCATGT AATTGAAAAT 600  
TACTGGAAAG CACTGGAAGA TGTAAGATTAT GTACAGACAT TTAAAGGATT AAAACTGAGA 660  
TTTGAACAAC AAAGAGAAAG GCAAGATAAT CCCAACTTG ACAGTATGCG TTCCATTTTG 720  
AGGAATCACA GATATCGAAG AGATGCCAGA AACTAGAAG ATGAAGAAGA GATGTGGTTT 780  
AACACAGATG AAGATGACAT GGAAGATGGA GAAGCTGTAG TGTCTCCATC TGACAAAAC 840  
AAAAATGATG ATGATATTAT GGATCCAATA AGTAAATTCA TGGAAAGGAA GAAATTAAAA 900

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GAAAGTGAGG AAAAGGAAGT GCTTCTGAAA ACAAACCTTT CTGGACGGCA GAGCCCAAGT  | 960  |
| TTCAAGCTTT CCCTGTCCAG TGGAACGAAG ACTAACCTCA CCAGCCAGTC ATCTACAACA  | 1020 |
| AATCTGCCTG GTTCTCCGGG ATCACCTGGA TCCCCAGGAT CTCCAGGCTC TCCTGGATCC  | 1080 |
| GTACCTAAAA ATACATCTCA GACGGCAGCT ATTACTACAA AGGGAGGCCT CGTGGGTCTG  | 1140 |
| GTAGATTATC CTGATGATGA TGAAGATGAT GATGAGGATG AAGATAAGGA AGATACGTTA  | 1200 |
| CCATTGTCAA AGAAAGCAAA ATTTGATTCA TAATAATGGC AACGGCCTAG GATCAGTACC  | 1260 |
| TGTTGAAAAA AACTGGTTCT CCACCCCTCC CCCATACAAA ATCCACAAAA AAGCGCAGTG  | 1320 |
| GTCTCTTG TG AATGACTGAC ACAGATCAGC CTCTTACACT TGACTTCTGC TCATCAAGTG | 1380 |
| CCAATTCAAT GGAGCAGGAG GAGGGGATAT CATATATTTA GGGGAAAGAC TTAAGCCTTT  | 1440 |
| GAGCTCTCCA GCTTGGACCA CACATTGCCC TTTTCTCAGG GAAGGAAATG GAAACAAAAA  | 1500 |
| GCCAACAGGG CAGGGGTTTT GTAAGTGGA CTCTGGATTG ACTGGTCAGT TGCTACAATC   | 1560 |
| AGAATATGCT TTCTTGACC ATGTTTGAGA CTCAGAAGAA TGGCCTTTCT GCCATAATTC   | 1620 |
| TTCCTAGTC AAGAATGCCA GCAGTTTCTT TGTATAAAGA GACCTGCCTT TAAAATCATA   | 1680 |
| CATTCTGAAC ATTTTAGTCA AGCTACAACA GGTTTGAAA ACCTCTGTGG GGGAGGGGCG   | 1740 |
| AGTATAAAGT TTTCTCTTT TTTAACTGTT CCCTTTGCCC TTCAAAGTGC AGATATTTTT   | 1800 |
| TTTTTTAAGT GGGGACTTCT CCCTACTTGA TTAAAGATTG AGTGGAATTC TAGATGTGGT  | 1860 |
| CATTTGTGTC ATAATTTTTT TGTTTTATTT TGTTTTTGAT TTTTTTTTTT CTCCCCTGAG  | 1920 |
| TGTATGCTTA GTTGTTGAGT ATATATATTT GGGACCATTA AAACCTTTTTT TGATGTAATA | 1980 |
| TAACCTAACG TTGTGCTGGT ACCTGTTTTA CCATGTGTAA TTTTGTCTT ACATCACAGT   | 2040 |
| TCTTAATTTG TTTAGAGTTT TATGAAAGAT GGTATAGTTT TTATTGACAA AAGCAAAGTA  | 2100 |
| ATCTTACAAC TATGTGCATA CAAAAGCAAT ACTATTTTGT GACTAAATAT TTTATATTAA  | 2160 |
| AATTTACATC AGCAACTGTC TTGAGAATTC AGGGAAATAG AATGGAATTT AAAACTTCAA  | 2220 |
| CAGTTTTGTT AAATCTAGAA ACATGAAATT RGTATTCCAA AGAGATTCTG AAATTTCTTT  | 2280 |
| TCTKGGGGAA ATGACGGTAC ATTAAATCAA AATTGRGGAT GGATGATTTA AAAACATTTG  | 2340 |
| ACTTTTTAAT AATAAAAAGA AAAGTGAAGA GTAAGAGAAA TTGTAAAAAA AAAAAAAAAA  | 2400 |
| AAAAAAAAA                                                          | 2409 |

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met Ile Cys Asp Thr Asp Pro Glu Leu Gly Gly Ala Val Gln Leu Met  
1 5 10 15

Gly Leu Leu Arg Thr Leu Val Asp Pro Glu Asn Met Leu Ala Thr Ala  
20 25 30

Xaa Lys Thr Xaa Lys Thr Glu Phe Leu Gly Phe Phe Tyr Lys His Cys  
35 40 45

Met His Val Leu Xaa Ala Pro Leu Leu Ala Asn Thr Thr Glu Asp Lys  
50 55 60

Pro Ser Lys Asp Asp Phe Gln Thr Ala Gln Leu Ala Leu Val Leu  
65 70 75 80

Glu Leu Leu Thr Phe Cys Val Glu His His Thr Tyr His Ile Lys Asn  
85 90 95

Tyr Ile Ile Asn Lys Asp Ile Leu Arg Arg Val Leu Val Leu Met Ala  
100 105 110

Ser Lys His Ala Phe Leu Ala Leu Cys Ala Leu Arg Phe Lys Arg Lys  
115 120 125

Ile Ile Gly Leu Lys Asp Glu Phe Tyr Asn Arg Tyr Ile Met Lys Ser  
130 135 140

Phe Leu Phe Glu Pro Val Val Lys Ala Phe Leu Asn Asn Gly Ser Arg  
145 150 155 160

Tyr Asn Leu Met Asn Ser Ala Ile Ile Glu Met Phe Glu Phe Ile Arg  
165 170 175

Val Glu Asp Ile Lys Ser Leu Thr Ala His Val Ile Glu Asn Tyr Trp  
180 185 190

Lys Ala Leu Glu Asp Val Asp Tyr Val Gln Thr Phe Lys Gly Leu Lys  
195 200 205

Leu Arg Phe Glu Gln Gln Arg Glu Arg Gln Asp Asn Pro Lys Leu Asp  
210 215 220

Ser Met Arg Ser Ile Leu Arg Asn His Arg Tyr Arg Arg Asp Ala Arg  
225 230 235 240

Thr Leu Glu Asp Glu Glu Glu Met Trp Phe Asn Thr Asp Glu Asp Asp  
245 250 255

Met Glu Asp Gly Glu Ala Val Val Ser Pro Ser Asp Lys Thr Lys Asn  
260 265 270

Asp Asp Asp Ile Met Asp Pro Ile Ser Lys Phe Met Glu Arg Lys Lys  
275 280 285

Leu Lys Glu Ser Glu Glu Lys Glu Val Leu Leu Lys Thr Asn Leu Ser  
290 295 300

Gly Arg Gln Ser Pro Ser Phe Lys Leu Ser Leu Ser Ser Gly Thr Lys

|                                                                 |                                                 |                         |     |     |  |     |
|-----------------------------------------------------------------|-------------------------------------------------|-------------------------|-----|-----|--|-----|
| 305                                                             |                                                 | 310                     |     | 315 |  | 320 |
| Thr Asn Leu Thr                                                 | Ser Gln Ser Ser Thr Thr                         | Asn Leu Pro Gly Ser Pro |     |     |  |     |
|                                                                 | 325                                             |                         | 330 |     |  | 335 |
| Gly Ser Pro Gly                                                 | Ser Pro Gly Ser Pro Gly Ser Pro Gly Ser Val Pro |                         |     |     |  |     |
|                                                                 | 340                                             |                         | 345 |     |  | 350 |
| Lys Asn Thr Ser Gln Thr Ala Ala Ile Thr Thr Lys Gly Gly Leu Val |                                                 |                         |     |     |  |     |
|                                                                 | 355                                             |                         | 360 |     |  | 365 |
| Gly Leu Val Asp Tyr Pro Asp Asp Asp Glu Asp Asp Asp Glu Asp Glu |                                                 |                         |     |     |  |     |
|                                                                 | 370                                             |                         | 375 |     |  | 380 |
| Asp Lys Glu Asp Thr Leu Pro Leu Ser Lys Lys Ala Lys Phe Asp Ser |                                                 |                         |     |     |  |     |
|                                                                 | 385                                             |                         | 390 |     |  | 395 |
|                                                                 |                                                 |                         |     |     |  | 400 |

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 951 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GCCAGGCAGG GTGTGGGGGC AGCTGTGCCA ATCTACCTCA CAGGCCACC CCCTGCCGGG   | 60  |
| CATGCCGTGG GATCATGGGC AGGGAAGGCT CTGGGGGTCTG GAGACACCGC TGCTTAGCAC | 120 |
| CCCCAGCCAG AACACCCTGA GGGTCTCGGG GCTCTGGAGA GAGTGGGGCG GGAGGAAGAA  | 180 |
| TTGGCACCTT CCTAGGGAAG GAGACGAGCG CTCGCCTTG ATTCTCCGAG AAGCCTCCGA   | 240 |
| GAAGTGCTTT AAGTGTGTTT GCATGCSCCA GCGGGTGGGC AGCGGGGGCC TGTCCARCCC  | 300 |
| TCTCCCGCCA TCCTTCCCCA AGTGACGTCC ACTGCCTTGT CACCAGCGAC CTGCCTGTCA  | 360 |
| TGCCCCACCC CTGAGGAAGC ATGGGGACCC TAACACCCTG GTGCCCTGCA CCAGACAGGC  | 420 |
| CGTGGTCAGG CCCAGGCCAC CGGCCGGGTT CTGCCACARC TTCCCACGTG CTTGCTGACA  | 480 |
| TGCSTGTGCC TGTGTGTGGT GTCTGTTGCT GTGTCGTGAA ACTGTGACCA TCACTCAGTC  | 540 |
| CAAACAAGTG AGTGGCCCTS GAGGCCACAG TTATGCAACT TTCAGTGTGT GTCATAACGA  | 600 |
| CGTCACTGCT TTTTAACTC GATAACTCTT TATTTTAGTA AAATGCCAG GAGTCCTGGA    | 660 |
| AGCTACGCGG ACTTGAGAG GTTTTATTTT TTGGCCTTAG AATCTGCAGA AATTAGGAGG   | 720 |
| CACCGAGCCC AGCGCAGCAG CCTCGGACCC GGATTGCGTT TGCCTTAGCG GATATGTTTA  | 780 |
| TACAGATGAA TATAAATGT TTTTCTTTT GGGCTTTTCTTCTTTT CCCCCCTTC          | 840 |
| TCACCTTCCC TTCTCCCTGA CCCCACCCCC CAAAAAGCT ACTTCTTCAT TCCGTGGTAC   | 900 |
| GATTATTTTT TTTAACTAAA GGAAGATAAA ATTCTAAAAA AAAAAAAAAA A           | 951 |

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

Met Pro Trp Asp His Gly Gln Gly Arg Leu Trp Gly Ser Glu Thr Pro
1 5 10 15
Leu Leu Ser Thr Pro Ser Gln Asn Thr Leu Arg Val Ser Gly Leu Trp
 20 25 30
Arg Glu Trp Gly Gly Arg Lys Asn Trp His Leu Pro Arg Glu Gly Asp
 35 40 45
Glu Arg Phe Ala Leu Ile Leu Arg Glu Ala Ser Glu Lys Cys Phe Lys
 50 55 60
Cys Val Cys Met Xaa Gln Ala Val Gly Ser Gly Gly Leu Ser Xaa Pro
65 70 75 80
Leu Pro Pro Ser Phe Pro Lys
 85

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(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1899 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

GGCCGCTTGT GTCCACGGGA CGCGGGCGGA TCTTCTCCGG CCATGAGGAA GCCAGCCGCT 60
GGCTTCCTTC CCTCACTCCT GAAGGTGCTG CTCCTGCCTC TGGCACCTGC CGCAGCCCAG 120
GATTCGACTC AGGCCTCCAC TCCAGGCAGC CCTCTCTCTC CTACCGAATA CGAACGCTTC 180
TTCGCACTGC TGA CTCCAAC CTGGAAGGCA GAGACTACCT GCCGTCTCCG TGCAACCCAC 240
GGCTGCCGGA ATCCCACACT CGTCCAGCTG GACCAATATG AAAACCACGG CTTAGTGCCC 300
GATGGTGCTG TCTGCTCCAA CCTCCCTTAT GCCTCCTGGT TTGAGTCTTT CTGCCAGTTC 360
ACTCACTACC GTTGCTCCAA CCACGTCTAC TATGCCAAGA GAGTCCTGTG TTCCCAGCCA 420
GTCTCTATTC TCTCACCTAA CACTCTCAAG GAGATAGAAG CTTCACTGA AGTCTCACCC 480
ACCACGATGA CCTCCCCCAT CTCACCCAC TTCACAGTGA CAGAACGCCA GACCTTCCAG 540
CCCTGGCCTG AGAGGCTCAG CAACAACGTG GAAGAGCTCC TACAATCCTC CTTGTCCCTG 600

```

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GGAGGCCAGG AGCAAGCGCC AGAGCACAAG CAGGAGCAAG GAGTGGAGCA CAGGCAGGAG  | 660  |
| CCGACACAAG AACACAAGCA GGAAGAGGGG CAGAAACAGG AAGAGCAAGA AGAGGAACAG  | 720  |
| GAAGAGGAGG GAAAGCAGGA AGAAGGACAG GGGACTAAGG AGGGACGGGA GGCTGTGTCT  | 780  |
| CAGCTGCAGA CAGACTCAGA GCCCAAGTTT CACTCTGAAT CTCTATCTTC TAACCCTTCC  | 840  |
| TCTTTTGCTC CCCGGGTACG AGAAGTAGAG TCTACTCCTA TGATAATGGA GAACATCCAG  | 900  |
| GAGCTCATTC GATCAGCCCA GGAAATAGAT GAAATGAATG AAATATATGA TGAGAACTCC  | 960  |
| TACTGGAGAA ACCAAAACCC TGGCAGCCTC CTGCAGCTGC CCCACACAGA GGCTTTGCTG  | 1020 |
| GTGCTGTGCT ATTCGATCGT GGAGAATACC TGCATCATAA CCCCCACAGC CAAGGCCTGG  | 1080 |
| AAGTACATGG AGGAGGAGAT CCTTGGTTTT GGGAAAGTCGG TCTGTGACAG CCTTGGGCGG | 1140 |
| CGACACATGT CTACCTGTGC CCTCTGTGAC TTCTGCTCCT TGAAGCTGGA GCAGTGCCAC  | 1200 |
| TCAGAGGCCA GCCTGCAGCG GCAACAATGC GACACCTCCC ACAAGACTCC CTTTGTGACG  | 1260 |
| CCCTTGCTTG CCTCCCAGAG CCTGTCCATC GGCAACCAGG TAGGGTCCCC AGAATCAGGC  | 1320 |
| CGCTTTTACG GGCTGGATTT GTACGGTGGG CTCCACATGG ACTTCTGGTG TGCCCGGCTT  | 1380 |
| GCCACGAAAG GCTGTGAAGA TGTCCGAGTC TCTGGGTGGC TCCAGACTGA GTTCCTTAGC  | 1440 |
| TTCCAGGATG GGGATTTCCC TACCAAGATT TGTGACACAG ACTATATCCA GTACCCAAAC  | 1500 |
| TACTGTTCCT TCAAAAGCCA GCAGTGTCTG ATGAGAAACC GCAATCGGAA GGTGTCCCGC  | 1560 |
| ATGAGATGTC TGCAGAATGA GACTTACAGT GCGCTGAGCC TGGCAAAAGT GAGGACGTTG  | 1620 |
| TGCTTTTCGAT GGAGCCAGGA GTTCAGCACC TTGACTCTAG GCCAGTTCGG ATGAGCTKGS | 1680 |
| GTTTATTTTG CCCACACCCC AGCCCAACCT GCCCASGTTT TCTATTGTTT TGAGACCCCA  | 1740 |
| TTGCTTTCAG GCTGCCCCCTT CTGGGTCTGT TACTCGGCCC CTAMTCACAT TTCCTTGGGT | 1800 |
| TGGAGCAACA GTCCCAGAGA GGGCCACGGT GGGAGCTGCG CCCTCCTTAA AAGATGACTT  | 1860 |
| TACATAAAAT GTTGATCTTC AAAAAAAAAA AAAAAAAAAA                        | 1899 |

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 543 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Lys | Pro | Ala | Ala | Gly | Phe | Leu | Pro | Ser | Leu | Leu | Lys | Val | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp Ser Thr Gln Ala Ser



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 20                                                              | 25  | 30  |
| Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr Glu Arg Phe Phe Ala |     |     |
| 35                                                              | 40  | 45  |
| Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr Cys Arg Leu Arg Ala |     |     |
| 50                                                              | 55  | 60  |
| Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln Leu Asp Gln Tyr Glu |     |     |
| 65                                                              | 70  | 75  |
| Asn His Gly Leu Val Pro Asp Gly Ala Val Cys Ser Asn Leu Pro Tyr |     |     |
| 85                                                              | 90  | 95  |
| Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr His Tyr Arg Cys Ser |     |     |
| 100                                                             | 105 | 110 |
| Asn His Val Tyr Tyr Ala Lys Arg Val Leu Cys Ser Gln Pro Val Ser |     |     |
| 115                                                             | 120 | 125 |
| Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu Ala Ser Ala Glu Val |     |     |
| 130                                                             | 135 | 140 |
| Ser Pro Thr Thr Met Thr Ser Pro Ile Ser Pro His Phe Thr Val Thr |     |     |
| 145                                                             | 150 | 155 |
| Glu Arg Gln Thr Phe Gln Pro Trp Pro Glu Arg Leu Ser Asn Asn Val |     |     |
| 165                                                             | 170 | 175 |
| Glu Glu Leu Leu Gln Ser Ser Leu Ser Leu Gly Gly Gln Glu Gln Ala |     |     |
| 180                                                             | 185 | 190 |
| Pro Glu His Lys Gln Glu Gln Gly Val Glu His Arg Gln Glu Pro Thr |     |     |
| 195                                                             | 200 | 205 |
| Gln Glu His Lys Gln Glu Glu Gly Gln Lys Gln Glu Glu Gln Glu Glu |     |     |
| 210                                                             | 215 | 220 |
| Glu Gln Glu Glu Glu Gly Lys Gln Glu Glu Gly Gln Gly Thr Lys Glu |     |     |
| 225                                                             | 230 | 235 |
| Gly Arg Glu Ala Val Ser Gln Leu Gln Thr Asp Ser Glu Pro Lys Phe |     |     |
| 245                                                             | 250 | 255 |
| His Ser Glu Ser Leu Ser Ser Asn Pro Ser Ser Phe Ala Pro Arg Val |     |     |
| 260                                                             | 265 | 270 |
| Arg Glu Val Glu Ser Thr Pro Met Ile Met Glu Asn Ile Gln Glu Leu |     |     |
| 275                                                             | 280 | 285 |
| Ile Arg Ser Ala Gln Glu Ile Asp Glu Met Asn Glu Ile Tyr Asp Glu |     |     |
| 290                                                             | 295 | 300 |
| Asn Ser Tyr Trp Arg Asn Gln Asn Pro Gly Ser Leu Leu Gln Leu Pro |     |     |
| 305                                                             | 310 | 315 |
| His Thr Glu Ala Leu Leu Val Leu Cys Tyr Ser Ile Val Glu Asn Thr |     |     |
| 325                                                             | 330 | 335 |
| Cys Ile Ile Thr Pro Thr Ala Lys Ala Trp Lys Tyr Met Glu Glu Glu |     |     |
| 340                                                             | 345 | 350 |

Ile Leu Gly Phe Gly Lys Ser Val Cys Asp Ser Leu Gly Arg Arg His  
355 360 365

Met Ser Thr Cys Ala Leu Cys Asp Phe Cys Ser Leu Lys Leu Glu Gln  
370 375 380

Cys His Ser Glu Ala Ser Leu Gln Arg Gln Gln Cys Asp Thr Ser His  
385 390 395 400

Lys Thr Pro Phe Val Ser Pro Leu Leu Ala Ser Gln Ser Leu Ser Ile  
405 410 415

Gly Asn Gln Val Gly Ser Pro Glu Ser Gly Arg Phe Tyr Gly Leu Asp  
420 425 430

Leu Tyr Gly Gly Leu His Met Asp Phe Trp Cys Ala Arg Leu Ala Thr  
435 440 445

Lys Gly Cys Glu Asp Val Arg Val Ser Gly Trp Leu Gln Thr Glu Phe  
450 455 460

Leu Ser Phe Gln Asp Gly Asp Phe Pro Thr Lys Ile Cys Asp Thr Asp  
465 470 475 480

Tyr Ile Gln Tyr Pro Asn Tyr Cys Ser Phe Lys Ser Gln Gln Cys Leu  
485 490 495

Met Arg Asn Arg Asn Arg Lys Val Ser Arg Met Arg Cys Leu Gln Asn  
500 505 510

Glu Thr Tyr Ser Ala Leu Ser Leu Ala Lys Val Arg Thr Leu Cys Phe  
515 520 525

Arg Trp Ser Gln Glu Phe Ser Thr Leu Thr Leu Gly Gln Phe Gly  
530 535 540

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 722 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CGACCTTCCC AGCAATATGC ATCTTGCACG TCTGGTCGGC TCCTGCTCCC TCCTTCTGCT | 60  |
| ACTGGGGGCC CTGTCTGGAT GGGCGGCCAG CGATGACCCC ATTGAGAAGG TCATTGAAGG | 120 |
| GATCAACCGA GGGCTGAGCA ATGCAGAGAG AGAGGTGGGC AAGGCCCTGG ATGGCATCAA | 180 |
| CAGTGAATC ACGCATGCCG GAAGGGAAGT GGAGAAGGTT TTCAACGGAC TTAGCAACAT  | 240 |
| GGGGAGCCAC ACCGGCAAGG AGTTGGACAA AGGCGTCCAG GGGCTCAACC ACGGCATGGA | 300 |
| CAAGGTTGCC CATGAGATCA ACCATGGTAT TGGACAAGCA GGAAAGGAAG CAGAGAAGCT | 360 |

TGGCCATGGG GTCAACAACG CTGCTGGACA GGGCAACCAT CAAAGCGGAT CTTCCAGCCA 420  
TCAAGGAGGG GCCACAACCA CGCCGTTAGC CTCTGGGGCC TCGGTCAACA CGCCTTTCAT 480  
CAACCTTCCC GCCCTGTGGA GGAGCGTCGC CAACATCATG CCCTAAACTG GCATCCGGCC 540  
TTGCTGGGAG AATAATGTCG CCGTTGTCAC ATCAGCTGAC ATGACCTGGA GGGGTTGGGG 600  
GTGGGGGACA GGTTTCTGAA ATCCCTGAAG GGGGTTGTAC TGGGATTTGT GAATAAACTT 660  
GATACACTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 720  
AA 722

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | His | Leu | Ala | Arg | Leu | Val | Gly | Ser | Cys | Ser | Leu | Leu | Leu | Leu | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gly | Ala | Leu | Ser | Gly | Trp | Ala | Ala | Ser | Asp | Asp | Pro | Ile | Glu | Lys | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ile | Glu | Gly | Ile | Asn | Arg | Gly | Leu | Ser | Asn | Ala | Glu | Arg | Glu | Val | Gly |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Lys | Ala | Leu | Asp | Gly | Ile | Asn | Ser | Gly | Ile | Thr | His | Ala | Gly | Arg | Glu |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Val | Glu | Lys | Val | Phe | Asn | Gly | Leu | Ser | Asn | Met | Gly | Ser | His | Thr | Gly |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Lys | Glu | Leu | Asp | Lys | Gly | Val | Gln | Gly | Leu | Asn | His | Gly | Met | Asp | Lys |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Val | Ala | His | Glu | Ile | Asn | His | Gly | Ile | Gly | Gln | Ala | Gly | Lys | Glu | Ala |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Glu | Lys | Leu | Gly | His | Gly | Val | Asn | Asn | Ala | Ala | Gly | Gln | Gly | Asn | His |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gln | Ser | Gly | Ser | Ser | Ser | His | Gln | Gly | Gly | Ala | Thr | Thr | Thr | Pro | Leu |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ala | Ser | Gly | Ala | Ser | Val | Asn | Thr | Pro | Phe | Ile | Asn | Leu | Pro | Ala | Leu |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |  |
| Trp | Arg | Ser | Val | Ala | Asn | Ile | Met | Pro |     |     |     |     |     |     |     |  |
|     |     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1240 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| AATGGCTTTT CTTCCTTCCT GGGTTTGTGT ACTAGTTGGT TCCTTTTCTG CTTCCTTAGC  | 60   |
| AGGGACTTCC AATCTCTCAG AGACAGAGCC CCCTCTGTGG AAGGAGAGTC CTGGTCAGCT  | 120  |
| CAGTGACTION AGGGTGGAGA ACAGCATGTA CATTATTAAT CCCTGGGTAT ACCTTGAGAG | 180  |
| AATGGGGATG TATAAAATCA TATTGAATCA GACAGCCAGG TATTTTGCAA AATTTGCACC  | 240  |
| AGATAATGAA CAGAATATTT TATGGGGGTT GCCTCTGCAG TATGGCTGGC AATATAGGAC  | 300  |
| AGGCAGATTA GCTGATCCAA CCCGAAGGAC AACTGTGGC TATGAATCTG GAGATCATAT   | 360  |
| GTGCATCTCT GTGGACAGTT GGTGGGCTGA TTTGAATTAT TTTCTGTCTT CATTACCCTT  | 420  |
| TCTTGCTGCG GTTGATTCTG GTGTAATGGG GATATCATCA GACCAAGTCA GGCTTTTGCC  | 480  |
| CCCACCCAAG AATGAGAGGA AGTTTGTGA TGATGTTTCT AGCTGTCGTT CATCCTTCCC   | 540  |
| TGAGACAATG AACAAGTGGA ACACCTTTTA CCAGTATTTG CAGTCACCTT TTAGTAAGTT  | 600  |
| TGATGATCTG TTGAAGTACT TATGGGCTGC ACACACTTCA ACCTTGGCAG ATAATATCAA  | 660  |
| AAGTTTTGAA GACAGATATG ATTATTATTC TAAAGCAGAA GCGCATTTTG AGAGAAGTTG  | 720  |
| GGTACTGGCT GTGGATCATT TAGCTGCAGT CCTCTTTCCT ACAACCTTGA TTAGATCATA  | 780  |
| TAAGTTCCAG AAGGGCATGC CACCACGAAT TCTTCTTAAT ACTGATGTAG CCCCTTTCAT  | 840  |
| CAGTGACTION ACTGCTTTTC AGAATGTAGT CCTGGTTCTT CTAAATATGC TTGACAATGT | 900  |
| GGATAAATCT ATAGGTTATC TTTGTACAGA AAAATCTAAT GTATATAGAG ATCATTCGGA  | 960  |
| ATCTAGCTCT AGAAGTTATG GAAATAACTC CTGAAACATT TAACTTCAAA CTTCAGGAAA  | 1020 |
| TGATTAATGA ATTAAAAATG AAAAAGCTCGA ACTTGACAAT CAGTAATTTT AAAAAATTAA | 1080 |
| TGTCATCATG ACCATGTAGT TTATTCTTTC TGATATTTTT GATTTATGCT TATTTGTTAA  | 1140 |
| GATCTTGTAC ATGTATTAAA AACTTAAATT AAATGCATTC AAGTTAAAAA AAAAAAAAAA  | 1200 |
| AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA                        | 1240 |

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 330 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Phe | Leu | Pro | Ser | Trp | Val | Cys | Val | Leu | Val | Gly | Ser | Phe | Ser | 1   | 5   | 10  | 15  |
| Ala | Ser | Leu | Ala | Gly | Thr | Ser | Asn | Leu | Ser | Glu | Thr | Glu | Pro | Pro | Leu | 20  | 25  | 30  |     |
| Trp | Lys | Glu | Ser | Pro | Gly | Gln | Leu | Ser | Asp | Tyr | Arg | Val | Glu | Asn | Ser | 35  | 40  | 45  |     |
| Met | Tyr | Ile | Ile | Asn | Pro | Trp | Val | Tyr | Leu | Glu | Arg | Met | Gly | Met | Tyr | 50  | 55  | 60  |     |
| Lys | Ile | Ile | Leu | Asn | Gln | Thr | Ala | Arg | Tyr | Phe | Ala | Lys | Phe | Ala | Pro | 65  | 70  | 75  | 80  |
| Asp | Asn | Glu | Gln | Asn | Ile | Leu | Trp | Gly | Leu | Pro | Leu | Gln | Tyr | Gly | Trp | 85  | 90  | 95  |     |
| Gln | Tyr | Arg | Thr | Gly | Arg | Leu | Ala | Asp | Pro | Thr | Arg | Arg | Thr | Asn | Cys | 100 | 105 | 110 |     |
| Gly | Tyr | Glu | Ser | Gly | Asp | His | Met | Cys | Ile | Ser | Val | Asp | Ser | Trp | Trp | 115 | 120 | 125 |     |
| Ala | Asp | Leu | Asn | Tyr | Phe | Leu | Ser | Ser | Leu | Pro | Phe | Leu | Ala | Ala | Val | 130 | 135 | 140 |     |
| Asp | Ser | Gly | Val | Met | Gly | Ile | Ser | Ser | Asp | Gln | Val | Arg | Leu | Leu | Pro | 145 | 150 | 155 | 160 |
| Pro | Pro | Lys | Asn | Glu | Arg | Lys | Phe | Cys | Tyr | Asp | Val | Ser | Ser | Cys | Arg | 165 | 170 | 175 |     |
| Ser | Ser | Phe | Pro | Glu | Thr | Met | Asn | Lys | Trp | Asn | Thr | Phe | Tyr | Gln | Tyr | 180 | 185 | 190 |     |
| Leu | Gln | Ser | Pro | Phe | Ser | Lys | Phe | Asp | Asp | Leu | Leu | Lys | Tyr | Leu | Trp | 195 | 200 | 205 |     |
| Ala | Ala | His | Thr | Ser | Thr | Leu | Ala | Asp | Asn | Ile | Lys | Ser | Phe | Glu | Asp | 210 | 215 | 220 |     |
| Arg | Tyr | Asp | Tyr | Tyr | Ser | Lys | Ala | Glu | Ala | His | Phe | Glu | Arg | Ser | Trp | 225 | 230 | 235 | 240 |
| Val | Leu | Ala | Val | Asp | His | Leu | Ala | Ala | Val | Leu | Phe | Pro | Thr | Thr | Leu | 245 | 250 | 255 |     |
| Ile | Arg | Ser | Tyr | Lys | Phe | Gln | Lys | Gly | Met | Pro | Pro | Arg | Ile | Leu | Leu | 260 | 265 | 270 |     |
| Asn | Thr | Asp | Val | Ala | Pro | Phe | Ile | Ser | Asp | Phe | Thr | Ala | Phe | Gln | Asn | 275 | 280 | 285 |     |
| Val | Val | Leu | Val | Leu | Leu | Asn | Met | Leu | Asp | Asn | Val | Asp | Lys | Ser | Ile | 290 | 295 | 300 |     |
| Gly | Tyr | Leu | Cys | Thr | Glu | Lys | Ser | Asn | Val | Tyr | Arg | Asp | His | Ser | Glu |     |     |     |     |

305

310

315

320

Ser Ser Ser Arg Ser Tyr Gly Asn Asn Ser  
325 330

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| GCAGCACCAG CCGTCTGCAG CTCCGGCCGC CACTTGCGCC TCTCCAGCCT CCGCAGGCCC | 60   |
| AACCGCCGCC AGCACCATGG CCAGCACCAT TTCCGCCTAC AAGGAGAAGA TGAAGGAGCT | 120  |
| GTCGGTGCTG TCGCTCATCT GTCCTGCTT CTACACACAG CCGCACCCCA ATACCGTCTA  | 180  |
| CCAGTACGGG GACATGGAGG TGAAGCAGCT GGACAAGCGG GCCTCAGGCC AGAGCTTCGA | 240  |
| GGTCATCCTC AAGTCCCCTT CTGACCTGTC CCCAGAGAGC CCTATGCTCT CCTCCCCACC | 300  |
| CAAGAAGAAG GACACCTCCC TGGAGGAGCT GCAAAAGCGG CTGGAGGCAG CCGAGGAGCG | 360  |
| GAGGAAGACG CAGGAGGCGC AGGTGCTGAA GCAGCTGGCG GAGCGGCGCG AGCACGAGCG | 420  |
| CGAGGTGCTG CACAAGGCGC TGGAGGAGAA TAACAACCTC AGCCGCCAGG CGGAGGAGAA | 480  |
| GCTCAACTAC AAGATGGAGC TCAGCAAGGA GATCCGCGAG GCACACCTGG CCGCACTGCG | 540  |
| CGAGCGGCTG CGCGAGAAGG AGCTGCACGC GGCCGAGGTG CGCAGGAACA AGGAGCAGCG | 600  |
| AGAAGAGATG TCGGGCTAAG GGCCCGGGAC GGGCGGCGCC CATCCTGCGA CAGAACACGT | 660  |
| TCGGGTTTTG GTTTTGTTC GTTCACCTCT GTCTAGATGC AACTTTTGTT CCTCCTCCCC  | 720  |
| CACCCAGCC CCCAGCTTCA TGCTTCTCTT CCGCACTCAG CCGCCCTGCC CTGTCCTCGT  | 780  |
| GGTGAGTCGC TGACCACGGC TTCCCCTGCA GGAGCCGCCG GCGGTGAGAC GCGGTCCCTC | 840  |
| GGTGCAGACA CCAGGCCGGG CGCGGTGGG TCCCCGGGG GCCCTGTGAG AGAGGTGGCG   | 900  |
| GTGACCGTGG TAAACCCAGG GCGGTGGCGT GGGATCGCGG GTCCTTACGC TGGGCTGTCT | 960  |
| GGTCAGCACG TGCAGGTCAG GGCAGGTCCT CTGAGCCGGC GCCCTGGCC AGCAGGCGAG  | 1020 |
| GCTACAGTAC CTGCTGTCTT TCCAGGGGGA AGGGGCTCCC CATGAGGGAG GGGCGACGGG | 1080 |
| GGAGGGGGGT GATGGTGCTT GGGAGCCTGC GTGTGCAGCC GGTGCTTGTT GAACTGGCAG | 1140 |
| GCGGGTGGGT GGGGGCTGCA GCTTTCCTTA ATGTGGTTGC ACAGGGGTCC TCTGAGACCA | 1200 |
| CCTGGCGTGA GGTGGACACC CTGGGCCTTC CTGGAAGCCT GCAGTTGGGG GCCTGCCCTG | 1260 |
| AGTCTGCTGG GGAGTGGGCA TTCTCTGCCA GGGACCCATG AGCAGGCTGC ATGGTCTAGA | 1320 |

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GGTTGTGGGC AGCATGGACA GTCCCCCACT CAGAAGTGCA AGAGTTCCAA AGAGCCTCTG 1380
GCCCAGGCCC CTCCCCACCA GGGCTTTGCA GATGTCCTTG AAAGACCCAC CCTAGAGCCC 1440
TTTGGAGTGC TGGCCCCCTCC TGTGCCCTCT GCCCTGGTGG AAGCGGCAGC CACAAGTCCT 1500
CCTCAGGGAG CCCCAAGGGG GATTTTGTGG GACCGCTGCC CACAGATCCA GGTGTTGGAA 1560
GGGCAGCGGG TAAGGTTCCC AAGCCAGCCC CAACACCCTT CCCACTTGGC ACCCAGAGGG 1620
GGCTGTGGGT GGAGGCCTGA CTCCAGGCCT CTCCTGCCCA CACCCTCTGG GCTGAGTTCC 1680
TTCTTTCCCT TGGACGCCCC GTGCTGGCCT TGGAGGACGG TCAGCTGGAG GATGGCGGTG 1740
GGGGAGGCTG TCTTTGTACC ACTGCAGCAT CCCCCACTTC TCCACGGAAG CCCCATCCCA 1800
AAGCTGCTGC CTGGCCCCCTT GCTGTAAAGT GTGAAGGGGG CGGCTGAGTT CTCTTAGGAC 1860
CCAGAGCCAG GGCCCTCAAC TTCCATCCTG CGGGAGGCCT TGGCCGGGCA CTGCCAGTGT 1920
CTTCCAGAGC CACACCCAGG GACCACGGGA GGATCCTGAC CCCTGCAGGG CTCAGGGGTC 1980
AGCAGGGACC CACTGCCCCA TCTCCCTCTC CCCACCAAGA CAGCCCCAGA AGGAGCAGCC 2040
AGCTGGGATG GGAACCCAAG GCTGTCCACA TCTGGCTTTT GTGGGACTCA GAAAGGGAAG 2100
CAGAACTGAG GGCTGGGATA TTCCTCATGG TGGCAGCGCT CATAGCGAAA GCCTACTGTA 2160
ATATGCACCC ATCTCATCCA CGTAGTAAAG TGAACTTAAA AATTCAATCA AATGAACAAT 2220
TAAATAAACA CCTGTGTGTT TAAGAAAAAA AAAAAAAAAA A 2261

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(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

Met Ala Ser Thr Ile Ser Ala Tyr Lys Glu Lys Met Lys Glu Leu Ser
1 5 10 15
Val Leu Ser Leu Ile Cys Ser Cys Phe Tyr Thr Gln Pro His Pro Asn
20 25 30
Thr Val Tyr Gln Tyr Gly Asp Met Glu Val Lys Gln Leu Asp Lys Arg
35 40 45
Ala Ser Gly Gln Ser Phe Glu Val Ile Leu Lys Ser Pro Ser Asp Leu
50 55 60
Ser Pro Glu Ser Pro Met Leu Ser Ser Pro Pro Lys Lys Lys Asp Thr
65 70 75 80
Ser Leu Glu Glu Leu Gln Lys Arg Leu Glu Ala Ala Glu Glu Arg Arg
85 90 95

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Lys Thr Gln Glu Ala Gln Val Leu Lys Gln Leu Ala Glu Arg Arg Glu  
100 105 110  
His Glu Arg Glu Val Leu His Lys Ala Leu Glu Glu Asn Asn Asn Phe  
115 120 125  
Ser Arg Gln Ala Glu Glu Lys Leu Asn Tyr Lys Met Glu Leu Ser Lys  
130 135 140  
Glu Ile Arg Glu Ala His Leu Ala Ala Leu Arg Glu Arg Leu Arg Glu  
145 150 155 160  
Lys Glu Leu His Ala Ala Glu Val Arg Arg Asn Lys Glu Gln Arg Glu  
165 170 175  
Glu Met Ser Gly  
180

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGCCAAAGAG GCCTAGGAGC CTCGTGGCTG CGTCACCGCC GCCCCCCCAG ACAAGATGGA | 60  |
| CACCGCGGAG GAAGACATAT GTAGAGTGTG TCGGTCAGAA GGAACACCTG AGAAACCGCT | 120 |
| TTATCATCCT TGTGTATGTA CTGGCAGTAT TAAGTTTATC CATCAAGAAT GCTTAGTTCA | 180 |
| ATGGCTGAAA CACAGTCGAA AAGAATACTG TGAATTATGC AAGCACAGAT TTGCTTTTAC | 240 |
| ACCAATTTAT TCTCCAGATA TGCCTTCACG GCTTCCAATT CAAGACATAT TTGCTGGACT | 300 |
| GGTTACAAGT ATTGGCACTG CAATACGATA TTGGTTTCAT TATACACTTG TGGCCTTTGC | 360 |
| ATGGTTGGGA GTTGTTCTC TTACAGCATG CCGCATCTAC AAGTGCTTGT TTAGTGGCTC  | 420 |
| CCGTGAGCTC ACTACTGACG CTGCCCATTG GATATGCTGT CAACCGGAAA ATTTGTTGGC | 480 |
| AGATTGTTTG CAGGGTTGTT TTGTGGTGAC GTGCACACTG TGTGCATTCA TCAGCCTGGT | 540 |
| GTGGTTGAGA GAGCAGATAG TCCATGGGGG AGCACCAATT TGGTTGGAGC ATGCTGCCCC | 600 |
| ACCGTTCAAT GCTGCGGGG ATCACCAAAA TGAGGCTCCA GCAGGAGGAA ATGGTGCAGA  | 660 |
| AAATGTTGCT GCTGATCAGC CTGCTAACCC ACCAGCTGAG AACGCAGTGG TGGGGGAAAA | 720 |
| CCCTGATGCC CAGGATGACC AGGCAGAAGA GGAGGAGGAG GACAATGAGG AGGAAGATGA | 780 |
| CGCTGGTGTG GAGGATGGCG GCAGATGCTA ATAACGGAGC CCAGGATGAC ATGAATTGGA | 840 |
| ATGCTTTAGA ATGGGACCGA GCTGCTGAAG AGCTTACATG GGAAAGAATG CTAGGACTTG | 900 |



|                                                                   |      |
|-------------------------------------------------------------------|------|
| ATGGATCACT AGTTTTTCTG GAACATGTCT TCTGGGTGGT ATCTTTAAAT ACACTGTTCA | 960  |
| TTCTTGTTTT TGCATTTTGC CCTTACCATA TTGGTCATTT CTCCCTTGTT GGTGGGAT   | 1020 |
| TTGAAGAACA CGTCCAAGCA TCTCATTTTG AAGGCCTAAT CACAACCATA GTTGGGTATA | 1080 |
| TACTTTTAGC AATAAACTG ATAATTTGTC ATGGCTTGGC AACTCTTGTC AAATTTTATA  | 1140 |
| GATCTCGTCG CTTACTGGGA GTCTGCTATA TTGTTGTTAA GGTCTCTTTG TTAGTGGTGG | 1200 |
| TAGAAATTGG AGTATTCCT CTCATTTGTG GTTGGTGGCT GGATATCTGT TCCTTGGA    | 1260 |
| TGTTTGATGC TACTCTGAAA GATCGAGAAC TGAGCTTTCA GTCGGCTCCA GGTACTACCA | 1320 |
| TGTTTCTGCA TTGGCTAGTG GGAATGGTAT ATGTCTTCTA CTTTGCCTCC TTCATTCTAT | 1380 |
| TACTGAGAGA GGTACTTCGA CCTGGTGTCC TGTGGTTTCT AAGGAATTTG AATGATCCAG | 1440 |
| ATTTCAATCC AGTACAGGAA ATGATCCATT TGCCAATATA TAGGCATCTC CGAAGATTTA | 1500 |
| TTTTGTCACT GATTGTCTTT GGCTCCATTG TCCTCTGAT GCTTTGGCTT CCTATACGTA  | 1560 |
| TAATTAAGAG TGTGCTGCCT AATTTTCTTC CATAAATGT CATGCTCTAC AGTGATGCTC  | 1620 |
| CAGTGAGTGA ACTGTCCCTC GAGCTGCTTC TGCTTCAGGT TGTCTTGCCA GCATTACTCG | 1680 |
| AACAGGGACA CACGAGGCAG TGGCTGAAGG GGCTGGTGCG AGCGTGGACT GTGACCGCCG | 1740 |
| GATACTTGCT GGATCTTCAT TCTTATTTAT TGGGAGACCA GGAAGAAAAT GAAAACAGTG | 1800 |
| CAAATCAACA AGTTAACAAT AATCAGCATG CTCGAAATAA CAACGCTATT CCTGTGGTGG | 1860 |
| GAGAAGGCCT TCATGCAGCC CACCAAGCCA TACTCCAGCA GGGAGGGCCT GTTGGCTTTC | 1920 |
| AGCCTTACCG CCGACCTTTA AATTTTCCAC TCAGGATATT TCTGTTGATT GTCTTCATGT | 1980 |
| GTATAACATT ACTGATTGCC AGCCTCATCT GCCTTACTTT ACCAGTATTT GCTGGCCGTT | 2040 |
| GGTTAATGTC GTTTTGGACG GGGACTGCCA AAATCCATGA GCTCTACACA GCTGCTTGTC | 2100 |
| GTCTCTATGT TTGCTGGCTA ACCATAAGGG CTGTGACGGT GATGGTGGCA TGGATGCCTC | 2160 |
| AGGGACGCAG AGTGATCTTC CAGAAGGTTA AAGAGTGGTC TCTCATGATC ATGAAGACTT | 2220 |
| TGATAGTTGC GGTGCTGTTG GCTGGAGTTG TCCCTCTCCT TCTGGGGCTC CTGTTTGAGC | 2280 |
| TGGTCATTGT GGCTCCCCTG AGGGTTCCCT TGGATCAGAC TCCTCTTTT TATCCATGGC  | 2340 |
| AGGACTGGGC ACTTGGAGTC CTGCATGCCA AAATCATTGC AGCTATAACA TTGATGGGTC | 2400 |
| CTCAGTGGTG GTTGAAAAT GTAATTGAAC AGGTTTACGC AAATGGCATC CGGAACATTG  | 2460 |
| ACCTTCACTA TATTGTTTCT AACTGGCAG CTCCCGTGAT CTCTGTGCTG TTGCTTTCCC  | 2520 |
| TGTGTGTACC TTATGTCATA GCTTCTGGTG TTGTTCTTT ACTAGGTGTT ACTGCGGAAA  | 2580 |
| TGCAAACTT AGTCCATCGG CGGATTTATC CATTTTACT GATGGTCGTG GTATTGATGG   | 2640 |
| CAATTTTGTG CTTCCAAGTC CGCCAGTTTA AGCGCCTTTA TGAACATATT AAAAATGACA | 2700 |
| AGTACCTTGK GGGTCAASGA CTCGGTGAAC TACGAACGGA AATCTGGGCA AACAAGGCTC | 2760 |

ATCTCCACCA CCTCCACAGT CATCCCAAGA ATAAAGTAGT TGTCTCAACA ACTTGACCTT 2820  
 CCCCTTTACA TGTCTTTTTT TGTGGACTTC TCTCTTKGGA GATTTTTTCCC AGTGATCTCT 2880  
 CAGCGTKGTT TTTAAGTTAA AKGTATTKGA CTTGTGTTCT CAGCATTCAG AGAGCAGCGG 2940  
 TGTAAGATTC TGCTGTTCTC CCTGGATCTT CTGACATKAC TGCTGTCTGA GATTTGTATA 3000  
 TGKGTAAATA CAAGTTCCTT GATACCCTAA AACCTTGGAT TAAACAGAAT GTGCATKGTA 3060  
 CATCTTTAAA CAAATGKAT ATTAATTTAT TAAAAA AAAA 3109

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Glu | His | Gln | Phe | Gly | Trp | Ser | Met | Leu | Pro | His | Arg | Ser | Met | 1   | 5   | 10  | 15  |
| Leu | Arg | Gly | Ile | Thr | Lys | Met | Arg | Leu | Gln | Gln | Glu | Glu | Met | Val | Gln | 20  | 25  | 30  |     |
| Lys | Met | Leu | Leu | Ile | Ser | Leu | Leu | Thr | His | Gln | Leu | Arg | Thr | Gln | 35  | 40  | 45  |     |     |
| Trp | Trp | Gly | Lys | Thr | Leu | Met | Pro | Arg | Met | Thr | Arg | Gln | Lys | Arg | Arg | 50  | 55  | 60  |     |
| Arg | Arg | Thr | Met | Arg | Arg | Lys | Met | Thr | Leu | Val | Trp | Arg | Met | Ala | Ala | 65  | 70  | 75  | 80  |
| Asp | Ala | Asn | Asn | Gly | Ala | Gln | Asp | Asp | Met | Asn | Trp | Asn | Ala | Leu | Glu | 85  | 90  | 95  |     |
| Trp | Asp | Arg | Ala | Ala | Glu | Glu | Leu | Thr | Trp | Glu | Arg | Met | Leu | Gly | Leu | 100 | 105 | 110 |     |
| Asp | Gly | Ser | Leu | Val | Phe | Leu | Glu | His | Val | Phe | Trp | Val | Val | Ser | Leu | 115 | 120 | 125 |     |
| Asn | Thr | Leu | Phe | Ile | Leu | Val | Phe | Ala | Phe | Cys | Pro | Tyr | His | Ile | Gly | 130 | 135 | 140 |     |
| His | Phe | Ser | Leu | Val | Gly | Leu | Gly | Phe | Glu | Glu | His | Val | Gln | Ala | Ser | 145 | 150 | 155 | 160 |
| His | Phe | Glu | Gly | Leu | Ile | Thr | Thr | Ile | Val | Gly | Tyr | Ile | Leu | Leu | Ala | 165 | 170 | 175 |     |
| Ile | Thr | Leu | Ile | Ile | Cys | His | Gly | Leu | Ala | Thr | Leu | Val | Lys | Phe | His | 180 | 185 | 190 |     |

Arg Ser Arg Arg Leu Leu Gly Val Cys Tyr Ile Val Val Lys Val Ser  
195 200 205

Leu Leu Val Val Val Glu Ile Gly Val Phe Pro Leu Ile Cys Gly Trp  
210 215 220

Trp Leu Asp Ile Cys Ser Leu Glu Met Phe Asp Ala Thr Leu Lys Asp  
225 230 235 240

Arg Glu Leu Ser Phe Gln Ser Ala Pro Gly Thr Thr Met Phe Leu His  
245 250 255

Trp Leu Val Gly Met Val Tyr Val Phe Tyr Phe Ala Ser Phe Ile Leu  
260 265 270

Leu Leu Arg Glu Val Leu Arg Pro Gly Val Leu Trp Phe Leu Arg Asn  
275 280 285

Leu Asn Asp Pro Asp Phe Asn Pro Val Gln Glu Met Ile His Leu Pro  
290 295 300

Ile Tyr Arg His Leu Arg Arg Phe Ile Leu Ser Val Ile Val Phe Gly  
305 310 315 320

Ser Ile Val Leu Leu Met Leu Trp Leu Pro Ile Arg Ile Ile Lys Ser  
325 330 335

Val Leu Pro Asn Phe Leu Pro Tyr Asn Val Met Leu Tyr Ser Asp Ala  
340 345 350

Pro Val Ser Glu Leu Ser Leu Glu Leu Leu Leu Leu Gln Val Val Leu  
355 360 365

Pro Ala Leu Leu Glu Gln Gly His Thr Arg Gln Trp Leu Lys Gly Leu  
370 375 380

Val Arg Ala Trp Thr Val Thr Ala Gly Tyr Leu Leu Asp Leu His Ser  
385 390 395 400

Tyr Leu Leu Gly Asp Gln Glu Glu Asn Glu Asn Ser Ala Asn Gln Gln  
405 410 415

Val Asn Asn Asn Gln His Ala Arg Asn Asn Asn Ala Ile Pro Val Val  
420 425 430

Gly Glu Gly Leu His Ala Ala His Gln Ala Ile Leu Gln Gln Gly Gly  
435 440 445

Pro Val Gly Phe Gln Pro Tyr Arg Arg Pro Leu Asn Phe Pro Leu Arg  
450 455 460

Ile Phe Leu Leu Ile Val Phe Met Cys Ile Thr Leu Leu Ile Ala Ser  
465 470 475 480

Leu Ile Cys Leu Thr Leu Pro Val Phe Ala Gly Arg Trp Leu Met Ser  
485 490 495

Phe Trp Thr Gly Thr Ala Lys Ile His Glu Leu Tyr Thr Ala Ala Cys  
500 505 510

Gly Leu Tyr Val Cys Trp Leu Thr Ile Arg Ala Val Thr Val Met Val

|                                                                 |     |             |
|-----------------------------------------------------------------|-----|-------------|
| 515                                                             | 520 | 525         |
| Ala Trp Met Pro Gln Gly Arg Arg Val Ile Phe Gln Lys Val Lys Glu |     |             |
| 530                                                             | 535 | 540         |
| Trp Ser Leu Met Ile Met Lys Thr Leu Ile Val Ala Val Leu Leu Ala |     |             |
| 545                                                             | 550 | 555 560     |
| Gly Val Val Pro Leu Leu Leu Gly Leu Leu Phe Glu Leu Val Ile Val |     |             |
|                                                                 | 565 | 570 575     |
| Ala Pro Leu Arg Val Pro Leu Asp Gln Thr Pro Leu Phe Tyr Pro Trp |     |             |
|                                                                 | 580 | 585 590     |
| Gln Asp Trp Ala Leu Gly Val Leu His Ala Lys Ile Ile Ala Ala Ile |     |             |
|                                                                 | 595 | 600 605     |
| Thr Leu Met Gly Pro Gln Trp Trp Leu Lys Thr Val Ile Glu Gln Val |     |             |
|                                                                 | 610 | 615 620     |
| Tyr Ala Asn Gly Ile Arg Asn Ile Asp Leu His Tyr Ile Val Arg Lys |     |             |
|                                                                 | 625 | 630 635 640 |
| Leu Ala Ala Pro Val Ile Ser Val Leu Leu Leu Ser Leu Cys Val Pro |     |             |
|                                                                 | 645 | 650 655     |
| Tyr Val Ile Ala Ser Gly Val Val Pro Leu Leu Gly Val Thr Ala Glu |     |             |
|                                                                 | 660 | 665 670     |
| Met Gln Asn Leu Val His Arg Arg Ile Tyr Pro Phe Leu Leu Met Val |     |             |
|                                                                 | 675 | 680 685     |
| Val Val Leu Met Ala Ile Leu Ser Phe Gln Val Arg Gln Phe Lys Arg |     |             |
|                                                                 | 690 | 695 700     |
| Leu Tyr Glu His Ile Lys Asn Asp Lys Tyr Leu Xaa Gly Gln Xaa Leu |     |             |
|                                                                 | 705 | 710 715 720 |
| Gly Glu Leu Arg Thr Glu Ile Trp Ala Asn Lys Ala His Leu His His |     |             |
|                                                                 | 725 | 730 735     |
| Leu His Ser His Pro Lys Asn Lys Val Val Val Ser Thr Thr         |     |             |
|                                                                 | 740 | 745 750     |

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TNTTTGAAGT TTCTCCCTCT CATTCTGAG

29

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GNTTCTCCAC GTAGTTGGTT TTCCTCAGT

29

- (2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CNACATGACG TGAGCTGGTG ATCCATGAA

29

- (2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ANTTGGGCTC TGCCGTCCAG AAAGGTTTG

29

- (2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GNAGCTACGC GGAATTGCAG AGGTTTTAT

29

- (2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TNGGTGAGAG AATAGAGACT GGCTGGGAA

29

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ANGAGCCGAC CAGACGTGCA AGATGCATA

29

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ANCTGACCAG GACTCTCCTT CCACAGAGG

29

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TNTAGGCGGA AATGGTGCTG GCCATGGTG

29

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:  
ANATATCCAG CCACCAACCA CAAATGAGA

29

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1425 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GCTAATTTGA GAAGAAAACA AGTAGGATTT TTGTTTTGTT TTGCATTTTG CAATATGGAG  | 60   |
| GAGAAATGAT TAGACCTTAG GAAGTGCCAG TGGGTTGGTC CTTTCATGAA CATGCCATCA  | 120  |
| GTAAAGCCC TGGAAACAAG GTCATACCAG AGATTTCATTG TGCCTTGTC CAACTGCAAA   | 180  |
| CAATATCTGA GTGGAATATT CAAAACTTG CTTAGAAAGA AAATCTAGG ACAGATGGCT    | 240  |
| CCACTGAAGT TATTCCAAAT ATTTAATAAA TAAAGCATAC CAGGCTTTTA TAACTCTTC   | 300  |
| TAGAAGAAAA AAGTTGGAAC TTTTCCAATT CAGTTTTTCA GGCCAGTGCA ACCTTGATAC  | 360  |
| CAAAACCAAT AAAACAAACA AACAAACAAA AAACATAAAG CTATAGACCA AAGTCTCATA  | 420  |
| GATTTAGATG CAAAATCCTA AAATTGAAAA AAAAAGTCTA GTCATATCCA TAACTGTAT   | 480  |
| CATCACCAAG AGATGTTTAT TAGGGCAATC AAAAGATGAT TTATTATTTT TAAAAAATC   | 540  |
| AATGTGGCCT TCCCTTCCTC TTTCTTTTGA TTCCCCTCTT TGAGTTTTTA TGTGTCTCTT  | 600  |
| TTGCCTTCCC TTCCCAGAGT GGAGGAGTTA GACCTGCATT GTGGGATGAG AGGAGTTGTG  | 660  |
| GCTATGTGTC TGCTGGCACC AAGAGGGGCTG AGGGTGAGGT GTGGAAGGGA CAGGGGGAGG | 720  |
| AGATGGGCAG CATTGTTAAG AGATTGGTAC CACTGAGCAA ATATGTTGAG AATGATGATG  | 780  |
| GCAAGGTTTC TCCCTGTTAG AGAAGGTATT TGTAGAAATA GGAATGAGGA GAGCTAGAAA  | 840  |
| ACCTGGAGTG TGGGATTAGA ATAGAACTCA TATCTTTTAA ATACATAGGA ACAATAGAGA  | 900  |
| AATTGTTGGG TGTGCCCATTA TACATATATT TTGTGATTCA TTCTACCGAG AGGACATAAA | 960  |
| TGCAGTCACA GCTCAGTAAC AGTAAACACA CCAACTGCCA AGTTATTATT TCCTAAATAC  | 1020 |
| TATCCACAAA AAAGGGGACC AGGGATGATT CCTAGTCGGA GATTGGGAGA AAAAGAAGAT  | 1080 |
| GAGCCTGAAT CATTTTCATGT ACCTAACAGA AAGAAAATAC TCTGGCTGGG CTCAGWGGCT | 1140 |
| CATGTTTGTA ATTCTAGCAT GTTAGGAGGT CGAGGTGGGT GTGTTGCTTG AGCCCAGGAG  | 1200 |

TTTGAGACCA GCCCAGGCAA CATGGCAAAA CTGTCTCTAC AAAAAATATA AAAGTTAGCC 1260  
 AGGCGTGGTG GCATGCGCCT GTCGTCCGAG ATACTCGGGA GGCAGAGAGG TGGGAGGATC 1320  
 ACTTGAGCCT GGGAGATTGA GACTGCATCG AGCTGTGGTC ATGCCACTGC ACTCCAGCCT 1380  
 GGAGGACAGA GTGAGACCCT GTCTCAGGAA AAAAAAAAAA AAAAA 1425

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met Ile Tyr Tyr Phe Leu Lys Asn Gln Cys Gly Leu Pro Phe Leu Phe  
 1 5 10 15  
 Leu Leu Ile Pro Leu Phe Glu Phe Leu Cys Val Ser Phe Ala Phe Pro  
 20 25 30  
 Ser Gln Ser Gly Gly Val Arg Pro Ala Leu Trp Asp Glu Arg Ser Cys  
 35 40 45  
 Gly Tyr Val Ser Ala Gly Thr Lys Arg Ala Glu Gly Glu Val Trp Lys  
 50 55 60  
 Gly Gln Gly Glu Glu Met Gly Ser Ile Val Lys Arg Leu Val Pro Leu  
 65 70 75 80  
 Ser Lys Tyr Val Glu Asn Asp Asp Gly Lys Val Ser Pro Cys  
 85 90

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2859 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CGCACCCAGC CGCGCCGGCG AGGACATGGG CAGCCGCGGC GCGCCCACCC CCCGCGCCGA 60  
 TGTGAATTAT TAAAAAGAAA ATGGCCCAAC GGAGCACTGT ATTTCTTCT CGTGTCACCA 120  
 AGGAAAGGTA TAATATATGG AAAATATGCA TCTAAGGCGA GTGAGAACCA TGCCCCGACA 180  
 CAGCCAGTCC CTGACCATGG CACCATACTC ATCTGTAAGC CTCGTGGAGC AGCTGGAAGA 240  
 CAGGATCCTC TGCCATGAGA AAACCACCGC CGCCCTCGTA GAGCACGCCT TTCGGATTAA 300  
 AGATGACATT GTCAACAGTT TGCAGAAAAT GCAAAACAAA GGGGGAGGTG ACCGCTTGGC 360



|                                                                   |      |
|-------------------------------------------------------------------|------|
| CAGGCTTTTC TTGGAGGAGC ATATCAGAAA CATAACTGCC ATAGTGAAGC AACTTAATCG | 420  |
| GGATATCGAG GTACTCCAGG AGCAGATTCG TGCTCGGGAC AACATTAGCT ATGGAACATA | 480  |
| TTCTGCCTTA AAGACCCTGG AGATGCGCCA GCTCTCCGGT TTGGGAGATC TTCGAGGAAG | 540  |
| AGTGGCAAGA TGTGATGCCA GCATAGCTAG ACTTTCTGCA GAGCACAAAA CGACCTATGA | 600  |
| GGGGCTCCAG CACTTGAACA AAGAACAGCA GGCTGCCAAA CTTATCTTGG AAACGAAAAT | 660  |
| CAAAGATGCA GAGGGACAGA TTTCTCAGCT TTTGAACAGA GTGGACTTGT CAATATCAGA | 720  |
| GCAGAGCACC AACTGAAGA TGTCTCACAG AGACAGTAAC CACCAGCTTC AGCTTTTGGA  | 780  |
| CACTAAATTT AAAGGTACAG TTGAGGAACT CAGTAACCAG ATATTATCTG CACGGAGTTG | 840  |
| GTTGCAACAG GAACAAGAAC GGATAGAAAA AGAGCTTTTA CAGAAAATTG ATCAGCTTTC | 900  |
| CTTGATTGTT AAGGAAAACA GTGGAGCCAG TGAAAGGGAT ATGGAGAAGA AGCTCAGCCA | 960  |
| GATGTCAGCC AGGCTTGACA AAATAGAAGA GGGTCAAAAG AAGACTTTTG ATGGTCAGAG | 1020 |
| AACAAGGCAA GAAGAGGAGA AGATGCACGG GCGAATCACC AAGCTGGAGT TACAGATGAA | 1080 |
| CCAGAACATC AAGGAAATGA AAGCAGAAGT TAATGCTGGG TTTACAGCCG TCTATGAAAG | 1140 |
| CATAGGATCC CTCAGGCAAG TTCTCGAGGC CAAGATGAAG CTGGACAGGG ACCAGCTACA | 1200 |
| GAAGCAAATC CAGCTGATGC AGAAGCCAGA GACCCCCATG TGAAGGGAGC TGGGACAAGG | 1260 |
| TCCTAAAAGA CAGTTTTGCC AGTGGGGCTA GGAGCCGGAT ACCTCTGTAG CCAGGCCATC | 1320 |
| GCTGCATTCA GGATTGTTCC ATCCATGGCG TGCATGTGCC AAGAAATGTG TTTTATGGG  | 1380 |
| TCTAAATGTT TACCTTGAGT CTTGAAAATA CTCTTTTGTT AAAAGTATGA AATACAGTTT | 1440 |
| TTACCAGTTT ATTTCACTTC TCTAAATTCA ATGGAAATCC CCCGCCCTGG ATTTTGAAAG | 1500 |
| GCTTTTATCT TCTTCATTTT ACGAATGGAA AGACGACAAT TTTTCTTCAA TGCTTGATGC | 1560 |
| ACTAATGAAG ACTGTTTACT ATTTTGAAAA ATGTCATGGG GATTTTTTTT TAATTAAGAA | 1620 |
| ACTAATGAAT CATCACAGGA ATGTGTTGCT CCTCACCCTA AATTAAGAGA ATGTCCCAGT | 1680 |
| AGATTAGACT TCAACCTTTG AGTCCAATTT GGATTTTATT ATCGTTGTCT ATGCACTTCT | 1740 |
| TATATTGGTT ATCTTCTTGT AAATCTTCTG TCTTTTGTA GGGGAAAGGA TTTAACATTT  | 1800 |
| AGAATAAACC CCACCATTTA TGTAATGGAA ATAGTTTAAA AATTGCTAAC TGCCATGTGG | 1860 |
| ATTGCAAATT AAATGGAAAC TTATTTAGAT AACGTAAGGC TCAATATCTG CGTTGACCAC | 1920 |
| CTAGATATTA CAGGTTTTAA TATTTAAAAC TATTTTGA TTTATCCACAA CCTGTATAGT  | 1980 |
| GATAGCCATA TATTTAATAA TGGAATGGTG GTTAACAGTC TATTTACTGC ACAATTAATT | 2040 |
| GTTCACTAAT CAAATAGAAT GTGGTAATTT TTCAGACTTT ATGATCTGTT TCCAAAATTG | 2100 |
| GCACAAAGTG CTAGGGTTTA TATACACTTA TCGTAACTGT ATTTTGTGC CTTGGTTTTA  | 2160 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TCATGTCAAT GCACTGTACT CTGTAAAAGT TTTGCAGACA AAATAGAAAG TATGATAATC  | 2220 |
| CGTCAGAAAGT ATGATGTAAA ACTGGAATCC TCTGTATTTT TTAAATGTTC TAAAAATTTT | 2280 |
| ATCGCTGTTA AGGTATTAAT CATTCAAGTAT TACTAATGGA ATAGAAATTC ATACTTTTGT | 2340 |
| ATGGACAACA AATTGATATT GCATTTATAG CACTGTAAGA AACTTTCATC TTGAGCAACT  | 2400 |
| TTGTAGATGA TGGGTGTTTT ATTTTCAATC GCCATATTTG ATCAGTCATT GAAAATTGGC  | 2460 |
| CCCAGTGCTG TTTGTTTCATC TCTGTATGTA AAAACTGACA GTGAGACACA ACTTTCTGAA | 2520 |
| CTGTGAGGGT GTCCCAGGAA AAAGAAAAAC AGGAATACTT TAACAATTAA AAAGAAAAAA  | 2580 |
| ATGTTTTTTTG TTTGCCAAGG ACTCAGGAAA ATAAAAAGCA TTTTCTATTT TTAGGACAAA | 2640 |
| TCACAAATGA AGTGTCTAAC TGGCTATTAC TGTTTACCCA TATAAAATAT GCTGCTAAAG  | 2700 |
| TACATATTTT GCTGTCAATG GCTTGACAAT TTTTTTTTTC AAATTGAGGAC ATGAGAGGTT | 2760 |
| ATATAGGGAC TATATTATCC AACACATATT TTCTTATTTT GCCACAAATT TCCACTTAAC  | 2820 |
| AAATAAAAAA AGGCGAATGC TGTTTTGCAA AAAAAAAA                          | 2859 |

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asn | Met | His | Leu | Arg | Arg | Val | Arg | Thr | Met | Pro | Arg | His | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Ser | Leu | Thr | Met | Ala | Pro | Tyr | Ser | Ser | Val | Ser | Leu | Val | Glu | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Glu | Asp | Arg | Ile | Leu | Cys | His | Glu | Lys | Thr | Thr | Ala | Ala | Leu | Val |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Glu | His | Ala | Phe | Arg | Ile | Lys | Asp | Asp | Ile | Val | Asn | Ser | Leu | Gln | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Met | Gln | Asn | Lys | Gly | Gly | Gly | Asp | Arg | Leu | Ala | Arg | Leu | Phe | Leu | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | His | Ile | Arg | Asn | Ile | Thr | Ala | Ile | Val | Lys | Gln | Leu | Asn | Arg | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Glu | Val | Leu | Gln | Glu | Gln | Ile | Arg | Ala | Arg | Asp | Asn | Ile | Ser | Tyr |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Thr | Asn | Ser | Ala | Leu | Lys | Thr | Leu | Glu | Met | Arg | Gln | Leu | Ser | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Gly | Asp | Leu | Arg | Gly | Arg | Val | Ala | Arg | Cys | Asp | Ala | Ser | Ile | Ala |

|                                                                 |     |             |
|-----------------------------------------------------------------|-----|-------------|
| 130                                                             | 135 | 140         |
| Arg Leu Ser Ala Glu His Lys Thr Thr Tyr Glu Gly Leu Gln His Leu |     |             |
| 145                                                             | 150 | 155 160     |
| Asn Lys Glu Gln Gln Ala Ala Lys Leu Ile Leu Glu Thr Lys Ile Lys |     |             |
|                                                                 | 165 | 170 175     |
| Asp Ala Glu Gly Gln Ile Ser Gln Leu Leu Asn Arg Val Asp Leu Ser |     |             |
|                                                                 | 180 | 185 190     |
| Ile Ser Glu Gln Ser Thr Lys Leu Lys Met Ser His Arg Asp Ser Asn |     |             |
|                                                                 | 195 | 200 205     |
| His Gln Leu Gln Leu Leu Asp Thr Lys Phe Lys Gly Thr Val Glu Glu |     |             |
|                                                                 | 210 | 215 220     |
| Leu Ser Asn Gln Ile Leu Ser Ala Arg Ser Trp Leu Gln Gln Glu Gln |     |             |
|                                                                 | 225 | 230 235 240 |
| Glu Arg Ile Glu Lys Glu Leu Leu Gln Lys Ile Asp Gln Leu Ser Leu |     |             |
|                                                                 | 245 | 250 255     |
| Ile Val Lys Glu Asn Ser Gly Ala Ser Glu Arg Asp Met Glu Lys Lys |     |             |
|                                                                 | 260 | 265 270     |
| Leu Ser Gln Met Ser Ala Arg Leu Asp Lys Ile Glu Glu Gly Gln Lys |     |             |
|                                                                 | 275 | 280 285     |
| Lys Thr Phe Asp Gly Gln Arg Thr Arg Gln Glu Glu Glu Lys Met His |     |             |
|                                                                 | 290 | 295 300     |
| Gly Arg Ile Thr Lys Leu Glu Leu Gln Met Asn Gln Asn Ile Lys Glu |     |             |
|                                                                 | 305 | 310 315 320 |
| Met Lys Ala Glu Val Asn Ala Gly Phe Thr Ala Val Tyr Glu Ser Ile |     |             |
|                                                                 | 325 | 330 335     |
| Gly Ser Leu Arg Gln Val Leu Glu Ala Lys Met Lys Leu Asp Arg Asp |     |             |
|                                                                 | 340 | 345 350     |
| Gln Leu Gln Lys Gln Ile Gln Leu Met Gln Lys Pro Glu Thr Pro Met |     |             |
|                                                                 | 355 | 360 365     |

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 933 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TGCTTCGGAG ACCGTAAGGA TATTGATGAC CATGAGATCC CTGCTCAGAA CCCCCTTCCT | 60  |
| GTGTGGCCTG CTCTGGGCCT TTTGTGCCCC AGGCGCCAGG GCTGAGGAGC CTGCAGCCAG | 120 |
| CTTCTCCCAA CCCGGCAGCA TGGGCCTGGA TAAGAACACA GTGCACGACC AAGAGTACGT | 180 |

ATTCAGCCCCG GGCTGTGGTC CAGTGGCCTC CCCATCATCT GCAGCTGAGC CAGCGGCAAG 240  
GGCATGCTCA GTCCTCCTTT CCTTCTTCCT GTTTCTATGG CTCCTTGACA TTCTTCAAGG 300  
ATGATTCTTA TTCCTTATTG CCACCTATAA GTCAGGTATT CTTTTTTCAT CATTGTATCA 360  
CAGGTGGAAG ATCTTTAGGC CCAAATGGGG CACATTACTT GTCTGAATCC GGTCTCTCCT 420  
TTTTTTCACC ACAGACAGAC ACACACACAT ACAAATAGAC ACACAGGTAC ACATACACAG 480  
TCATAGTAGC AGAATCCAGA AAATAGCTAA GGTTTCTTGA CTATAACAAG ACCTTTTTTTA 540  
AATCAACACA TTCAAACATT GAATCATTTG TTGCAGCTTT TGTCTTGGGC CAGTTAGCCT 600  
CACGCATTAT ACTCGGTTAT CCTTTGTTTT TAAGGCTGGG TGCAGTGGCT CACACCTGTA 660  
ATCCCAGTGC TTTGGGAGGC TGAGGCAGGT GGATTACTTG AGCCCAGGAA TTCGAGACCA 720  
GCCTAGGCAA TATAGGGAAA ACCTGTCTCT AYTAATAAAT TGCAATAAAT TAGCTGGATG 780  
TGGCAGTACA TGCCTATGGT CCCAGCTACT TGGGGGGCTG AAGTGGGAGA ATCAAMTGAG 840  
CTTGGGAAGT TGAGGCTACA ATGAGCCAAG ATCAGCTCC TGCACTCCAG CCTGGGTGGC 900  
AGAGTGAGAC CCTGTCTCAA AAAAAAAAAA AAA 933

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 92 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met Thr Met Arg Ser Leu Leu Arg Thr Pro Phe Leu Cys Gly Leu Leu  
1 5 10 15  
Trp Ala Phe Cys Ala Pro Gly Ala Arg Ala Glu Glu Pro Ala Ala Ser  
20 25 30  
Phe Ser Gln Pro Gly Ser Met Gly Leu Asp Lys Asn Thr Val His Asp  
35 40 45  
Gln Glu Tyr Val Phe Ser Pro Gly Cys Gly Pro Val Ala Ser Pro Ser  
50 55 60  
Ser Ala Ala Glu Pro Ala Ala Arg Ala Cys Ser Val Leu Leu Ser Phe  
65 70 75 80  
Phe Leu Phe Leu Trp Leu Leu Asp Ile Leu Gln Gly  
85 90

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2956 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| GGTGTGTGGT GGTTTAAGAA TGTATATCAT AGGGTCAGGT GGCCTGGGTT CATTCCCCAG | 60   |
| CTACGTAACC TTTCTATGCC TGAGTTTCCT CATCTATAAA ACAAGGATAA TAATAGTGTG | 120  |
| TACTTCTTAG GATTGTTTTG GAGACTCATA AATGAGAAAT ACGTGAAAAA CTCCCTCAAG | 180  |
| GCAGTGCTTG ACACATAATG AGCACTCAGT TATCATGGTC ATCATGGTCA TCATCACTGC | 240  |
| TACCACCACT GCTGCTGCTA TTACCACTCT ACCTCTTCCC CCTGAAACTC TAATCACTTA | 300  |
| CCCTAGAAAC AGTTAAATTA CACTTCAGTG GGAAGGATCT CAGATTTCTT AATGGCACCT | 360  |
| GCATTTATAT AATGTTGATA TTGCACGTTT CTAGAAAACA TATCAAGAAG AAACCAAAAT | 420  |
| GTGTTTCTGT ACTTTGTAAA CCTGTACAAT AGTTAGAGAT TAGAGGACCT TTATAATCTA | 480  |
| CTACTAATTA CTGTGAAAGT AAACATTGTT TAATATACCA GTTCTTAAAG AAATATTTTG | 540  |
| TCTAGTCATT AATATTCTAG TTCATCTCAA AGCTTCCATT TGACAATTTA AAATTACTTA | 600  |
| AATTTTAATA TTAAAGGAAA CAGTTTTCCT GATTCTCATG AAAGTTCCTA TTTGCACTGA | 660  |
| AGATGACTAA ACCTTTTAGT CATAGTTTGA GAAGAATTGG CTTTTTTATA GCCATTTTAT | 720  |
| TTACATATGG GTACTGCATA GCAAAGGCAG CAGATTAGCC CTGTTTGTTT TGCAGGGATG | 780  |
| AAAGGTAGCA TTCCCAGAGA TTAAGTTGTT CTGCTATTC CCATTCTCTG CTACATTTCG  | 840  |
| CTACATTCTT TGGTCCTTTC TATTATTTGT TTCTTTGGTG GAATCCCCTT GTTGCTTATG | 900  |
| GCTGGATATT GTTATTCAGC AGATGAATCA CAAGTTTAGC CTGAGGGCCC TAAAGCATCA | 960  |
| GAAATAAATT AGAGCCGAGC AAAGTTTAAC TTCTCTGGAA CTTGCACCTT TAGTTTCCAT | 1020 |
| GTATTTCTGG AACCAAGATA TTTCAAAGGC TTACTTTATT TCAGACACCT ATTATCTTCA | 1080 |
| AGTCACAGAT AACTATTGAT TCTGTAAAGT GTTTCAAAGA TTTTGTCCA CTAGACATTT  | 1140 |
| TTAAATTTGT TCAACTCCTC CTCATCATTT TAGAAATTAT TTCTGTTAGG TAAAATTAAA | 1200 |
| ACTAACAATG TATTTTAGTT TATTTTCTA ATGATACCAG TCACCTTTCG GGGCTAACTA  | 1260 |
| AACATTTTGT GCAGCATTCT CTTAGTTTAC ATCCTCCTTT CTTTCAGTCT TCCTGTTTAT | 1320 |
| TAAGGCTGTC CTGTAGCAAA CAAAAGAGTG ACTCATGTTA AAAGTATTTT AACTGCTCTA | 1380 |
| ATATATCTGA GGAAGAATAA CTTTCTAAAT TAAAGTAATG TATTTTATTA AATATTAAAA | 1440 |
| TGCATTTTTT GGCTATTCAT TTCTGTATGT AAAAGAAAAG TTAACCTTAT GGTGTTATGC | 1500 |
| AAAATATGCT AAATTTAGAT TTTAGAGCAA TATATAGGGA GATATGTCAC AAATTTCTAC | 1560 |
| ATTTTGGTTA AATTATTAGT ATTTTCTTAT ATTCAAATGT GCCTTGATAT TTAAATAATA | 1620 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| TACTGAATGC AGAATTTATG TTATGTGAAC CATTATGGAA AATGTTAATG TTAACAAAAT | 1680 |
| GAGGTGTATT GACTTTTCAA CAATGTAAAT TAAAGATGGT ACATCTACTG TTTAAGGGCA | 1740 |
| GAGGAATTAA AAGAGTATAG ATACTGAAAT GTATCACTTA CTAGTAGTGT GGCTATAATC | 1800 |
| AAATTAATTA ATCTCTCTCT AGGCTTTAGC TTCCTCATCT TAGTTTGTTT AGGCTACTGT | 1860 |
| AACAAAATAA CATAGATTAT GTACTTTTAA ATGACAGAAG TTTATTCGGC ATGGTTTGGG | 1920 |
| AGACTAGGAA GTCTAAGATT AAAGAACCAG CAAATTTGGT GTCTGATGAG GACCCATTCC | 1980 |
| TTTGTTTACA GATGATGCCT TCTCATTGTG TTTTCAAATG TTAGAAGGAG CTAGCTAGCT | 2040 |
| TTCTGGGGTC TCTTTTGTA AGGCACTAAT CCCAGTCATT AGGGCAAATT GGCTCCTACA  | 2100 |
| GGCCCCACCT ATCTCCTAAT ACCATCACCT TGAGGATTAA GATTTCTACA TATGAATGAA | 2160 |
| GCAGGTGTTG TAGAAGGTCA GTCAGTTAGA CCATAGCACC ATCTGTAAAA TTGAATAGTA | 2220 |
| ATTTACTGCC TCATTGGATG TCAGGATTAA AGGAGATAAG ATTTTATTAG TTACTAGTTA | 2280 |
| CCATAGTGGT TTTTTTTTTT CACTATAATG TTCGTTTTTT TGTTCATGC TTGTACCTTC  | 2340 |
| AACATTTCTT TCCATTTGAA TACTTCTTTT GTCTCCTGTA GGCCTGTCTG TCCACTTAGG | 2400 |
| TGTAAGATGT GTTTTTGTGT CAGGAATGAT GGTGCAATGC TAATGTTCCA TTGCCCTATT | 2460 |
| TGGCAATACT CTGATCATT ACTATAAAGA ATAACACCAG TGTTAACTAA CTCTCCTTGC  | 2520 |
| CTGACAGTAG TGCTGCCACT ATTCCTTGTT TCTGTGGTAA TAGATGAGGT TTGTATGGTC | 2580 |
| CTGTTATTCC AGCCTCCAGA CACCATTCCA GATCAACTGG TGCCYTCWAC GCCCCGAAG  | 2640 |
| TGTATGGGGC CTCAGGTGAA GGATGAGWAC ATTTTCACTA TCATCTGGCA TTCATCTCAG | 2700 |
| ATTTTATCCT TTTCAGTTT CATTAAATAA TATTCATGTT TTAAAATTGA TTTTTATTA   | 2760 |
| TTTAAATTTA ATTTGTTGGA GAATAAACTT TTTTTTTTCT TTTCTCCCAA GTAACGTTTT | 2820 |
| CCCCTTTAGC AACTGTATTG AGCATTTTTT TCACTGGTAT ATGGACATTT TTTTGTATAA | 2880 |
| CCTGTTGTGT CATTTTAAAA TATAGAATTG TTTTATGTT CTCATCTTTG TATATATGTT  | 2940 |
| TAAAAAATAA AAAAAA                                                 | 2956 |

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Lys | Pro | Phe | Ser | His | Ser | Phe | Arg | Arg | Ile | Gly | Phe | Phe | Ile |
| 1   |     |     |     |     |     |     |     |     | 10  |     |     |     |     | 15  |     |

Ala Ile Leu Phe Thr Tyr Gly Tyr Cys Ile Ala Lys Ala Ala Asp  
20 25 30

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| AATCGGGAAA AAAAGCCATG TATTCTTTTCG TTTCTCTCTA AAAGAAGAAA AATATAATTT | 60   |
| AAAAATACAT TCGGTATTTT CTAAAACAAT AAATTTATAG TGTTAATATT CATAGGGTCA  | 120  |
| ATCAAAATGA AGCTTCTCCT TTGGGCTGC ATTGTATGTG TTGCTTTTGC AAGGAAGAGA   | 180  |
| CGGTTCCCCT TCATTGGTGA GGATGACAAT GACGATGGTC ACCCACTTCA TCCATCTCTG  | 240  |
| AATATTCCTT ATGGCATACG GAATTTACCA CCTCCTCTTT ATTATCGCCC AGTGAATACA  | 300  |
| GTCCCCAGTT ACCCTGGGAA TACTTACACT GACACAGGGT TACCTTCGTA TCCCTGGATT  | 360  |
| CTAACTTCTC CTGGATTCCC CTATGTCTAT CACATCCGTG GTTTTCCCTT AGCTACTCAG  | 420  |
| TTGAATGTTC CTCCTCTCCC TCCTAGGGGT TTCCCGTTTG TCCCTCCTTC AAGGTTTTTT  | 480  |
| TCAGCAGCTG CAGCACCCGC TGCCCCACCT ATTGCAGCTG AGCCTGCTGC AGCTGCACCT  | 540  |
| CTTACATCCA CACCTGTAGC ATCTGAGCCT GCTGCAGGGG CCCCTGTTGC AGCTGAGCCT  | 600  |
| GCTGCAGAGG CACCTGTTGG AGCTGAGCCT GCTGCAGAGG CACCTGTTGC AGCTGAGCCT  | 660  |
| GCTGCAGAGG CACCTGTTGG AGTGGAGCCA GCTGCAGAGG AACCTTCACC AGCTGAGCCT  | 720  |
| GCTACAGCCA AGCCTGCTGC CCCAGAACCT CACCCTTCTC CCTCTCTTGA ACAGGCAAAT  | 780  |
| CAGTGAAATT CTCTAGAAGA GTACCATGGG TTCATTTCTA TACTGATGCA GAAATAAGTG  | 840  |
| AAATCTACAA AAGTTTTCTT TCTTTTCCAA AGACTATTTT ATTCTGTAGT ATTCAGAGTA  | 900  |
| TTCATCTCAC TACATAGATT TGTTTGTGGT AGTTATTTCC TTGGACTTAA TTTATATTGA  | 960  |
| AAAAACATTG ATAATTAAAT AAATAAAATA GATAATTTAG ACCAATGGTG ATAAGGTCTG  | 1020 |
| GATGAAACT ACGCTATGGA GGACTGAAAT GGCAATCATT CAGCCTAGCC TGGAGTCTGA   | 1080 |
| TTATACAGCT ACTATAGGAT GATGTTAGTA TTGGTTTTGA GTGCAATAGG TTTTTCCTA   | 1140 |
| AACAAACATA TTTTGTAGTC AATGAACTTT TTGTCACAAA ACAGTAAAAC ATCTGTGTTT  | 1200 |
| AACCTATGGT AAACAACATG TTAATGAACT ATGCTATCCA TGACTTAATG GACAGTTCAA  | 1260 |
| AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA   | 1320 |
| AAAAA                                                              | 1325 |

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```

Met Lys Leu Leu Leu Trp Ala Cys Ile Val Cys Val Ala Phe Ala Arg
 1 5 10 15
Lys Arg Arg Phe Pro Phe Ile Gly Glu Asp Asp Asn Asp Asp Gly His
 20 25 30
Pro Leu His Pro Ser Leu Asn Ile Pro Tyr Gly Ile Arg Asn Leu Pro
 35 40 45
Pro Pro Leu Tyr Tyr Arg Pro Val Asn Thr Val Pro Ser Tyr Pro Gly
 50 55 60
Asn Thr Tyr Thr Asp Thr Gly Leu Pro Ser Tyr Pro Trp Ile Leu Thr
65 70 75 80
Ser Pro Gly Phe Pro Tyr Val Tyr His Ile Arg Gly Phe Pro Leu Ala
 85 90 95
Thr Gln Leu Asn Val Pro Pro Leu Pro Pro Arg Gly Phe Pro Phe Val
 100 105 110
Pro Pro Ser Arg Phe Phe Ser Ala Ala Ala Ala Pro Ala Ala Pro Pro
 115 120 125
Ile Ala Ala Glu Pro Ala Ala Ala Ala Pro Leu Thr Ser Thr Pro Val
 130 135 140
Ala Ser Glu Pro Ala Ala Gly Ala Pro Val Ala Ala Glu Pro Ala Ala
 145 150 155 160
Glu Ala Pro Val Gly Ala Glu Pro Ala Ala Glu Ala Pro Val Ala Ala
 165 170 175
Glu Pro Ala Ala Glu Ala Pro Val Gly Val Glu Pro Ala Ala Glu Glu
 180 185 190
Pro Ser Pro Ala Glu Pro Ala Thr Ala Lys Pro Ala Ala Pro Glu Pro
 195 200 205
His Pro Ser Pro Ser Leu Glu Gln Ala Asn Gln
 210 215

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(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TGCGGGCTCA CANGAANAGT CTCACCTCAG TGCCAAGGGG TGTCAGAGAT GCTCACTGCC | 60  |
| CTCCTCTCCT TGGGGTTGCA TGNAGGCATG ATGGCGCTTG GCCGTGGCAG GGTAAGGAAC | 120 |
| CGGCGACNGA GGCCCATCAC GTGTTACAT GCTCTCCTGC GTCNGTGCTT GGGAGATATG  | 180 |
| GACTGTCNTG TCCTTAGACC ACATTTATNT CAAGGCAAGG GGAGC                 | 225 |

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GGTTCAAAAT GAGGCAAAGA TAGGAAAGTG CTTCTTACAG ATAATTTTCA AGGCCAGTGA  | 60  |
| CTGGAGAGAG GGGTAGGTCT GTCAATCGAG TGCTTGCTGA CTGCACATAT CACAGGGCGT  | 120 |
| GTGACGACTG CTGGGAGAGG AAAGCGAGAC ATCATTCCAA CCCTCCAGAA GCTAAAGATC  | 180 |
| CTGGAACTCA AGGGGAAAAC TAACGTAAGT GCGAAAGCGA ACAAGCAAAC ATGTCTCTCA  | 240 |
| CGGGGCAGGC AGGCTGTCTGG GGTACAGAGC TGGGATCTGG GAAGGAACAG AGAGGGCCGC | 300 |
| TCAGGGAGAG GAAGCACAGT GCCACCGGAG GCACGCACTC AGCAGGCACT CGCAGGCTGG  | 360 |
| GCAGAGGTAG AGAAGCAGCG CTGCACAGGC AGGCAGCTGA CCCAGGGCTC TTAGAGCCGG  | 420 |
| GCAGGAGAGC TGGTGTGGGA CCTGGGAGGA GGACAGGAGC CTTCAAAGCA GCACCGCCTG  | 480 |
| ATTGCAGCCA GGAGGGTAGC ATCAAGGAAG ATGGAAGTGC GGCCAGGCCA CAT         | 533 |

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Thr | Gly | Gln | Ala | Gly | Cys | Arg | Gly | Thr | Glu | Leu | Gly | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gly | Lys | Glu | Gln | Arg | Gly | Pro | Leu | Arg | Glu | Arg | Lys | His | Ser | Ala | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Gly Gly Thr His Ser Ala Gly Thr Arg Arg Leu Gly Arg Gly Arg Glu  
 35 40 45  
 Ala Ala Leu His Arg Gln Ala Ala Asp Pro Gly Leu Leu Glu Pro Gly  
 50 55 60  
 Arg Arg Ala Gly Val Gly Pro Gly Arg Arg Thr Gly Ala Phe Lys Ala  
 65 70 75 80  
 Ala Pro Pro Asp Cys Ser Gln Glu Gly Ser Ile Lys Glu Asp Gly Thr  
 85 90 95  
 Ala Ala Arg Pro His  
 100

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 458 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

TAGGCAGTCA TCTTTGTAAA CCTCCACTGG TGCTGGCTGC GTTTAGAACA TACTCCATAT 60  
 AAAACAGGCC CTGGGATTAC AGGCATGAGC TACCGTGCCT GGCCCCCTTT TTTTAAATTA 120  
 CAGAGAAATA AGTTACACCT TAGTATCAGA TATTAATTTT CTTCAAGTGT CAGGCAATTA 180  
 GTATTTAGAA AGCTCTTGTC ATGAGATGGC TCTGGGATGT GATGATGATT GTTGGGATTG 240  
 AAAAAATGGT AGTATCATGG AGAGATCATA ATAAATTCTT AGTATTAAAA GTGGTTTTGC 300  
 TTTCAAGTTAG GGAGAAAAAT TAGATTGTAC TATTTTTCCT CTATGATTTC CTTCAAGTTAT 360  
 CTTCCAAATG TTGTTTTTTC CCCACAGCCC CCTTAACATT GTTCTCTATG CACTTCTCAA 420  
 TACATTTTCA TTTGTTTCTC AAAAAAAAAA AAAAAAAAAA 458

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1350 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TTTTTTTTTT TTTTGTAGA GACAGGGTCT TGCCATTTTG CCCAGGTTGG TCTCAAACCTT 60  
 CTGAGCTCAG GCTATCTGCC CACCTTGGCC TCCCAAAGTG CTGGGATTAC AGGTGTGAGC 120  
 CACTGTGCCC GGCCTGTATT GTTTTAAGTT ACACTTATTC CTTTAAAAAT TCAGAATTTG 180

TTAAGCATTT AAAACAAATT CATAAATTAA AACCTCCTTG AGATACCATT TACCATGTAG 240  
 TTTGATGAAC ATAATACATG GTGCATTACA TTGGCAAAAG CAGTGGGGAA AAAGATGCTT 300  
 TTATAAATGT CTGGTGGGAG TTAAATTGTG TAACTTCTAT TACACTTTTG TAATAGCTAC 360  
 CAAAATATGT TATTTCTATC TACCTCTCTC TCTCTGACTC AACAGTTCCA TTTCTAGGTT 420  
 TTGTGTTGTG GATATTCTTG AACATTGTGA AATGTATACA GGGAGGCTTC ACAGCAGCAC 480  
 TGTTTGTTTC AAATGATTTG AAAACAACCT CTCCATAAAC GAGATAGGCT AAATCAAGCA 540  
 TGGCACACCT ATACAATGGA TCGGGCCATT AAAAAGAACA AGGCAGCTCA TATGCATCAA 600  
 TATAAAAAGG TCTATAAACT ATACTATCAA ATGAAAATAG CAAGATGCTA CCATTTATAT 660  
 TAAAAAGAGG ACAAATATT AATATATTCA TGGTTGCTTG TCTATGTGGA ATATTTCTGG 720  
 ATATATACAT AAGAAGTTAC ATTGGTTACC TATGGGCAGG TTACTACTGG GTGGCTTGTG 780  
 GGTGAGGGCA GGAAGAGCTT ACTTTCCATG GTAAACCTTT TTGTATATTT TGCAGCATTC 840  
 AAAAATTCTA ATTTAAAGTT TATTTTAGAA AAATGCCCCC ATGTATACAA GTGATTTCCA 900  
 AGTTCCTCCT TCAATATTTT TAATGATTAT GGAACACACT GAACTTCTTT TTTATTATTC 960  
 TAGCTGTGAA CTCTGTCTGC TGTCTACATG CACATATATA ATCTATGTAA TATTTAAATT 1020  
 TATATCCTTT ATATGTCAGT TGGGTGGTGA GTAAAGAAA AATATATTTT TATCAGCAAA 1080  
 CTTGGTAAAT TGTTGAGGTT TCTGATATAG TCAGAGGTAG TTGCTTATCA CAACATTAGG 1140  
 TAAGTTTTTA AARACACCTA TTAAAACAC ACTGATGTAT ATATATATTG GTCTGTTTTT 1200  
 ATGCTGCTGA TAAAGACATA TCCAAGACTG GGAAGAAAAA GAGGTTTAAT TGGGCTTATA 1260  
 GTTCCACATG GCTGGGGAGG CCTCAGAATC ATTGCGGGAG GCAAAAGGCA CTTCTTACAT 1320  
 GGCAGTGGCA AGAGAAAAAA AAAAAAAAAA 1350

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 46 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Leu Pro Phe Ile Leu Lys Arg Gly Gln Asn Ile Asn Ile Phe Met  
 1 5 10 15  
 Val Ala Cys Leu Cys Gly Ile Phe Leu Asp Ile Tyr Ile Arg Ser Tyr  
 20 25 30  
 Ile Gly Tyr Leu Trp Ala Gly Tyr Tyr Trp Val Ala Cys Gly  
 35 40 45

## (2) INFORMATION FOR SEQ ID NO:113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

|                                                                      |      |
|----------------------------------------------------------------------|------|
| TCGGGACACT ACATGAAGTC CTGAAAATAA CAGAGAAACT GTTATATCTT TTTAATGATT    | 60   |
| TATTTGCAAG TATTGAGGTT GACCTGAAAA ACAATGAAAC ACATGAACAC ACTTCCGATT    | 120  |
| TTCTCCTCGC TGATTAGCTT CCTGCCTGCT GTCAGTGCTG GACGAAGTGC TATAACTACT    | 180  |
| TTATGTAACA TTACAGAACA GCTAGAGGTC CTGGGGTAAG AGAAAAAAAG CACATCACAA    | 240  |
| CAAATGTGAA AGCCTTCATT ATTACACGTT CCAGTTTGTC TCGCTGTGTA GGCATAAGCT    | 300  |
| AATGGTTTAT TTTCAGAAAG CTGCCTGAAA CGTTGCTTTG TATTCTTCTA GGAAGAACTT    | 360  |
| TAATTCCTCC TGAGGAACTC TACTTTCTGA GCCAACTGC TAATTTTCTG CGGAACTGTC     | 420  |
| TAGAAGATCA TTCAAGAGAC CCTGCAGTTG CACTTTCTCG TAAAGTTAA AAAAAAAAAA     | 480  |
| AAAAAAAAAG GTTTTCCCG GCCTTTGAAC ATTTTGCCTA TGAGAGTTTT GCATATATTT     | 540  |
| TATACTTGAG TAGACAACTT TAATAATCCA TATTTATACT ATCGCAGAAG TAAGCATTTG    | 600  |
| GCAAACGTTT AGCCATTAGC ACTCATTTAA CCCTGTTAGC AATATTCTTT TGAAAAAAGT    | 660  |
| GCCAGTCCTT ATGTGATAAA CTAAGAAGCC CATTGAATAT AAAANTGTGT NGGACTGAAA    | 720  |
| CNGTGACCTT ATATTATTGC TAAGGGAATA TGAGATTAAAC TTCCTACAGG GGCCANAACC   | 780  |
| ANANAAAGGC TTCCAGCAAC TTCGATNAAA NTANTTTGGC CACATNTCAA GCCAATTGTT    | 840  |
| TGTACTATTT ATGTACCTTT TTCATAACTG GAATTGCCAA ATAAGCATGG AGATCTAAAT    | 900  |
| GRAAAAAAAA AAAAAAAAAA AAAGCGGCCG CAGGTCTAGA ATTCAATCGG AAAAAACAAA    | 960  |
| GAGAAGAAAC ATACTGCCCC ATCTTGTTTG CATGAACTC TAGAATCTGG TGTTTCTCTA     | 1020 |
| TTTATCTGCT CCCTCTTTGC CTACCTTGGN ATTTCTTTTT TTTTTCTTT GTAACTATGG     | 1080 |
| TTTTTACCTA AAGTTTAAAC TTTTATTAT TATTTTCTCT CTAAATTCTT GCTAGTTAAT     | 1140 |
| AACATTATTA ACTTCAAGAT TTTAGAAGAG CAGTGATGAT AGTAATGATC GATAACTAGA    | 1200 |
| CTATCGAGTT TCAGAAGAAA CTTCCAAGTA TATATAATGT TTGACATAGC CTTTATTTCT    | 1260 |
| ACAAATCTAC TACCTGTAAA CTAACATTTT AAAATACCTG TATATGGCTG GGTGTGGTGG    | 1320 |
| CTTACACCTG TAATCCCAGC AGTTTGGGAG CCTGAGGTGG GCAGATTGCT TGAGCCCAGG    | 1380 |
| AGTTGGAGAC AAGCCTGGAC AAAATAGACC TCTCTCTACA AAAAGTACAA AAAATTGGCT    | 1440 |
| GGGTGTGGTG GCACACGCCT GTGGTCCCAG CTA CTCTCGGGA GGCTGAGGTG GGAGGATTGC | 1500 |

CTGAGCCCGG GAGATGGTGG TTGCAGTGAG CTGAGATCAC CCCATTGCAC TCCAGCCTGG 1560  
ATAACAGAAT AAGATGCTGT CTTAAAAAAA AAAAAAAA 1598

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Lys His Met Asn Thr Leu Pro Ile Phe Ser Ser Leu Ile Ser Phe  
1 5 10 15  
Leu Pro Ala Val Ser Ala Gly Arg Ser Ala Ile Thr Thr Leu Cys Asn  
20 25 30  
Ile Thr Glu Gln Leu Glu Val Leu Gly  
35 40

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1257 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CATGGCGTCC AGGTCTAAGC GCGTGCCGT GGAAAGTGGG GTTCCGCAGC CGCCGGATCC 60  
CCCAGTCCAG CGCGACGAGG AAGAGGAAAA AGAAGTCGAA AATGAGGATG AAGACGATGA 120  
TGACAGTGAC AAGGAAAAGG ATGAAGAGGA CGAGGTCATT GACGAGGAAG TGAATATTGA 180  
ATTTGAAGCT TATTCCTAT CAGATAATGA TTATGACGGA ATTAAGAAAT TACTGCAGCA 240  
GCTTTTTCTA AAGGCTCCTG TGAACACTGC AGAACTAACA GATCTCTTAA TTCAACAGAA 300  
CCATATTGGG AGTGTGATTA AGCAAACGGA TGTTTCAGAA GACAGCAATG ATGATATGGA 360  
TGAAGATGAG GTTTTTGGTT TCATAAGCCT TTAAATTTA ACTGAAAGAA AGGGTACCCA 420  
GTGTGTTGAA CAAATTCAAG AGTTGGTTMT ACGCTTCTGT GAGAAGAAGT GTGAAAAGAG 480  
CATGGTTGAA CAGCTGGACA AGTTTTTAAA TGACACCACC AAGCCTGTGG GCCTTCTCCT 540  
AAGTGAAAGA TTCATTAATG TCCCTCCACA GATCGCTCTG CCCATGTACC AGCAGCTTCA 600  
GAAAGAAGT KCGGGGGCAC ACAGAACCAA TAAGCCATGT GGGAAAGTGCT ACTTTTACCT 660  
TCTGATTAGT AAGACATTTG TGGAAGCAGG AAAAAACAAT TCCAAAAAGA AACCTAGCAA 720

CAAAAAGAAA GCTGCGTTAA TGTTTGCAAA TGCAGAGGAA GAATTTTCT ATGAGAAGGC 780  
AATTCTCAAG TTCAACTACT CAGTGCAGGA GGAGAGCGAC ACTTGTCTGG GAGGCAAATG 840  
GTCTTTTGAT GACGTACCAA TGACGCCCTT GCGAACTGTG ATGTTAATTC CAGGCGACAA 900  
GATGAACGAA ATCATGGATA AACTGAAAGA ATATCTATCT GTCTAACCCA TTTCCAATGG 960  
ACAGTGATGG GCTTGTTTTT GTAAAATTAC CAGAAAACCTC AGTGGAGATT TACTGAAAAA 1020  
CTCAGACTTT ATTCAGATTA AGTTCCTCTA CAAAAAGTAG GGTCTGTCC CATGTGTYTC 1080  
TGACACATTT ACAAATACC AGTTTTTTAA AATTTTGGTC AAATTATGAG TGGTTGATTT 1140  
AAAAACTTTT CCAAGAAGAA GAAAGCATG GAGTAGTAAT TTAAAGAACT CAATAAAAAAC 1200  
TTCTATTTTT TATTTTAAAA TAATAAAAAA AAAAAAAAAA AAAAAA 1257

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met Ala Ser Arg Ser Lys Arg Arg Ala Val Glu Ser Gly Val Pro Gln  
1 5 10 15  
Pro Pro Asp Pro Pro Val Gln Arg Asp Glu Glu Glu Glu Lys Glu Val  
20 25 30  
Glu Asn Glu Asp Glu Asp Asp Asp Ser Asp Lys Glu Lys Asp Glu  
35 40 45  
Glu Asp Glu Val Ile Asp Glu Glu Val Asn Ile Glu Phe Glu Ala Tyr  
50 55 60  
Ser Leu Ser Asp Asn Asp Tyr Asp Gly Ile Lys Lys Leu Leu Gln Gln  
65 70 75 80  
Leu Phe Leu Lys Ala Pro Val Asn Thr Ala Glu Leu Thr Asp Leu Leu  
85 90 95  
Ile Gln Gln Asn His Ile Gly Ser Val Ile Lys Gln Thr Asp Val Ser  
100 105 110  
Glu Asp Ser Asn Asp Asp Met Asp Glu Asp Glu Val Phe Gly Phe Ile  
115 120 125  
Ser Leu Leu Asn Leu Thr Glu Arg Lys Gly Thr Gln Cys Val Glu Gln  
130 135 140  
Ile Gln Glu Leu Val Xaa Arg Phe Cys Glu Lys Asn Cys Glu Lys Ser  
145 150 155 160

Met Val Glu Gln Leu Asp Lys Phe Leu Asn Asp Thr Thr Lys Pro Val  
165 170 175

Gly Leu Leu Leu Ser Glu Arg Phe Ile Asn Val Pro Pro Gln Ile Ala  
180 185 190

Leu Pro Met Tyr Gln Gln Leu Gln Lys Glu Leu Xaa Gly Ala His Arg  
195 200 205

Thr Asn Lys Pro Cys Gly Lys Cys Tyr Phe Tyr Leu Leu Ile Ser Lys  
210 215 220

Thr Phe Val Glu Ala Gly Lys Asn Asn Ser Lys Lys Lys Pro Ser Asn  
225 230 235 240

Lys Lys Lys Ala Ala Leu Met Phe Ala Asn Ala Glu Glu Glu Phe Phe  
245 250 255

Tyr Glu Lys Ala Ile Leu Lys Phe Asn Tyr Ser Val Gln Glu Glu Ser  
260 265 270

Asp Thr Cys Leu Gly Gly Lys Trp Ser Phe Asp Asp Val Pro Met Thr  
275 280 285

Pro Leu Arg Thr Val Met Leu Ile Pro Gly Asp Lys Met Asn Glu Ile  
290 295 300

Met Asp Lys Leu Lys Glu Tyr Leu Ser Val  
305 310

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GCGGTCCTGC CACACAAGCT GGGCGGCGGA GGCCACGCAG CCGGGCCTTC TTCTCTCTGG  | 60  |
| GACCCTCCGC CAGCGCATAG CCGCAGGCCG GTGTGACTTC TGCACCCTCG GTTCTGAGGG  | 120 |
| TACGGTGACC CCTAGTGGGC AGTTTGCAAA ATGTGATTCC TTCTTCCCAA CTCCCCATCC  | 180 |
| CCCCTTCCCT TCCCGTCACG TCCTGTTTGG GGGTTAATTC GGTTTTTTCT CTGTTGCATC  | 240 |
| GCGCCTACTG TGC GTGTGCG ATARCGTGTG TGGGGGTGAG AGTTTGTTTT CTGGAATGGT | 300 |
| AGGTGCTGGG AGGAGGAGTT TGATGGAGGG CTTCTGGCT GCTTCTGGCC CTCACCTCGT   | 360 |
| GGAGGCCTTC ACAGAGACCC TGTGGGCCCT GGCCCTGTGC TGGCACTGTG CCAGTCATGA  | 420 |
| GGCAGCTCTG ATCACTTCCC CACTGTGGAA ACAGGACTGA CCCAGCCTTC AGTGTGGGCT  | 480 |
| GCTGAAGCTA TCCTCCTCAG GCCTCAGGGA TGACCTCTCG CCTGAGCCTC TCACAGGCTG  | 540 |
| GCTGTGGGCC AGTTTCATCT GCTTTCCTGT TGGGGGTCCC GGGCCTCTGC TGTCTTGAC   | 600 |

CCACTGGTGT TCTGTGCAAG GCTTCTTCCC ATTCACCAAG TGCACACCTT GCATCTGCCG 660  
 CTCGGCATGC ACCAGTTCCA CACACCATCC CATTTTACAG ACAAGGACGC TGAGGCCTGC 720  
 AGCAGCAGTG TGA CTTGCTC AAGGTCCAGT GAGTGACCTC ATTCCCCAGA AAAGGCTCCT 780  
 CCCACACCAG AGTACAGCCT GGGTAGGGGG AAAATCAGTT CTTTCAGCTA CCACCCATCC 840  
 AACCTTTGGG CCTATGTGAA AAGAAAGGAA CTAAGCTGGG TGTGTTCTGT CTGGACCTGG 900  
 GGAGGCCCCCT GAAGGCAAAG AGGGAAACTG TCCCAGCTGT TCTGTCCTAG GGGAGGGGGA 960  
 CATAGCCCTA GCAGGAGCTC CCAGCCCCTC TTGGCACTCT GACACACAAG TACACCCATC 1020  
 TGGGGCCCGC TTTGCCACGA AGAGCTGGGC AGGCCTGCAG GGTGTGGGGA AGGAGGACAC 1080  
 AACCTCAAGA AAGGAAGCGT GAACCCCAAG GAACAGCGGG TCCCTTCCCT CCTCAGACAC 1140  
 AAGCCACCTC AGCTTGTGGC TCTTGGCCCC CAGCCCCACC AACCCACCTG TTCATTTATT 1200  
 CAACAGACAA TGACAGCTGA TATTTATTGG ACATTTGCAC CATGCCAAGC ATTCGGCTTG 1260  
 GATTATCCCA TTTGTTTCTC ACAGCCGGTA TTTATTGTCT GCTCCTCTGT GCCAGGTGCT 1320  
 GTGCTCTGGG CAGGGGCACT GCATGGGCTG CCTGCCCTGG TGGAGCTTGT GGTCTGATGG 1380  
 GTGAGGCTGA CCAAGCCCA CCCATTGCC AACAGGGCCA GGGCAAGAGT ACACACAGGG 1440  
 GCCTCATACC ATATGTCTAA ATATTTAAAA GTTATCAATC AAGCTAACA CTGTAAATA 1500  
 AAATATGTTT TATTCTCCTA CTTTGAAAAA AAAAAAAAAA AAAA 1544

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 72 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Met Pro Ser Ile Arg Leu Gly Leu Ser His Leu Phe Leu Thr Ala Gly  
 1 5 10 15  
 Ile Tyr Cys Leu Leu Cys Ala Arg Cys Cys Ala Leu Gly Arg Gly  
 20 25 30  
 Thr Ala Trp Ala Ala Cys Pro Gly Gly Ala Cys Gly Leu Met Gly Glu  
 35 40 45  
 Ala Asp Pro Ser Pro Pro His Cys Gln Gln Gly Gln Gly Lys Ser Thr  
 50 55 60  
 His Arg Gly Leu Ile Pro Tyr Val  
 65 70

(2) INFORMATION FOR SEQ ID NO:119:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CNATGCAGGTC TAACTCCTCC ACTCTGGG

29

- (2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TNAGTTTGGTG CTCTGCTCTG ATATTGAC

29

- (2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GNCATCAATAT CCTTACGGTC TCCGAAGC

29

- (2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GNAAATAGGAA CTTTCATGAG AATCAGGA

29

- (2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ANACAATGCAG GCCCAAAGGA GAAGCTTC

29

- (2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GNTTGCTTGTT CGCTTTCGCA CTTACGTT

29

- (2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ANTGGTAGCAT CTTGCTATTT TCATTGTA

29

- (2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

TNGGAAGTGTG TTCATGTGTT TCATTGTT

29

- (2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GNCCTCGTCCT CTTATCCTT TTCCTTGT

29

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ANCACCTGGCA CAGAGGAGCA GACAATAA

29

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GGCGAGCCTT TGAGGGGAAC GACTTGTCGG AGCCCTAACC AGGGGTATCT CTGAGCCTGG 60  
 TGGGATCCCC GGAGCGTCAC ATCACTTTC GATCACTTCA AAGTGTAAGG GGGGCCCTAC 120  
 TGACCCTTGG AATTTAGGGG GGCTACCCTA GGCGGCATCC ACAACAGAGA GAATTCCTT 180  
 GGAGAGGGGA CCCTGGTGCT CGGCTGTCCC TCTCATCCGC GTAGAAAGTC CCTCATCTGG 240  
 GGGCTCCCGA ACTCAGCCCT CTCACATTGT GGCCGGCTTT ACTGACCCTC ACAGACCCAG 300  
 GCTGGGCCCT CCCGATAGAG GCCAGCCAAA GGTTCACCTA GCCTCTCTTT CAAGGCTGGT 360  
 GTATCTCTAA ATCTTAGACC CTCCTCCGTT ACCGTCAGCC AGGTGGGATG CCCACGTTT 420  
 GGAGAGAAAC CGTTCTGAGG AACCCGGGCC TCTGGGTCCC AGCTGGCTCT CCGGCCCCCA 480  
 GGTATGTAT TCTGGGTGG CCACAAACAG TGGAATTCTA GGCACCTCCG GGACAGGGTG 540  
 GGAAGCTGTG CCTCATTCAT GCAACCAGCA AATATTCACG GCACCTTGTT TGTGCCAGAC 600  
 AGCAGACCGA GGACACGGTT GTTACCAAGA CCAGGCTGTT GCCTTGGAAG AGCCCAGAGC 660  
 GTGTCAAGGG AGACAGCCAC ATCAGGCCAG AAATACATGA CAGCTGGATT AGCCCTGGGA 720  
 GAGGGAGGCC CAGATGTGGG AGCTCAGGGG AGGTGCAGCT CAACGTGGAG TTTGGAGGAG 780  
 GCTACCTTGA CTTTGAATG CCAAGTGGGA GCCAGCCAGA TGAAAGGGGT TAAAACTAA 840  
 TATTTATATG ACAGAAAGAA AAGATGTCAT TCCGTAAAGT AAACATCATC ATCTTGGTCC 900  
 TGGCTGTTGC TCTCTTCTTA CTGTTTTTGC ACCATAACTT CCTCAGCTTG AGCAGTTTGT 960  
 TAAGGAATGA GGTACAGAT TCAGGAATTG TAGGGCCTCA ACCTATAGAC TTTGTCCCAA 1020  
 ATGCTCTCCG ACATGCAGTA GATGGGAGAC AAGAGGAGAT TCCTGTGGTC ATCGCTGCAT 1080  
 CTGAAGACAG GCTTGGGGGG GCCATTGCAG CTATAAACAG CATTACAGAC AACACTCGCT 1140  
 CCAATGTGAT TTTCTACATT GTTACTCTCA ACAATACAGC AGACCATCTC CCGTCCTGGC 1200  
 TCAACAGTGA TTCCCTGAAA AGCATCAGAT ACAAATTGT CAATTTTGAC CCTAACTTT 1260

|            |             |             |            |             |            |      |
|------------|-------------|-------------|------------|-------------|------------|------|
| TGGAAGGAAA | AGTAAAGGAG  | GATCCTGACC  | AGGGGGAATC | CATGAAACCT  | GTGATATTCT | 1320 |
| TGCCCTTTAC | AATACAGCAC  | TGAAGCCAGG  | ACATGCAGCT | GCATTTTCAG  | AAGATTGTGA | 1380 |
| TTCAGCCTCT | ACTAAAGTTG  | TCATCCGTGG  | AGCAGGAAAC | CAGTACAATT  | ACATTGGCTA | 1440 |
| TCTTGACTAT | AAAAAGGAAA  | GAATTTCGTAA | GCTTTCCATG | AAAGCCAGCA  | CTTGCTCATT | 1500 |
| TAATCCTGGA | GTTTTTGTG   | CAAACCTGAC  | GGAATGGAAA | CGACAGAATA  | TAACTAACCA | 1560 |
| ACTGGAAAAA | TGGATTCAAT  | TCAATGTAGA  | AGAGGGACTG | TATAGCAGAA  | CCCTGGCTGG | 1620 |
| TAGCATACAC | ACACCTCCTC  | TGCTTATCGT  | ATTTTATCAA | CAGCACTCTA  | CCATCGATCC | 1680 |
| TATGTGGAAT | GTCCGCCACC  | TTGGTTCCAG  | TGCTGGAAAA | CGATATTCAC  | CTCAGTTTGT | 1740 |
| AAAGGCTGCC | AAGTTACTCC  | ATTGGAATGG  | ACATTTGAAG | CCATGGGGAA  | GGACTGCTTC | 1800 |
| ATATACTGAT | GTTTGGGAAA  | AATGGTATAT  | TCCAGACCCA | ACAGGCCAAAT | TCAACCTAAT | 1860 |
| CCGAAGATAT | ACCGAGATCT  | CAAACATAAA  | GTGAAACAGA | ATTTGAACTG  | TAAGCAAGCA | 1920 |
| TTTCTCAGGA | AGTCCTGGAA  | GATAGCATGC  | GTGGGAAGTA | ACAGTTGCTA  | GGCTTCAATG | 1980 |
| CCTATCGGTA | GCAAGCCATG  | GAAAAAGATG  | TGTCAGCTAG | GTAAAGATGA  | CAAACCTGCC | 2040 |
| TGCTCGGCAG | TCAGGTTCCC  | AGACGAGACTA | TAGACTATAA | ATATGTCCTC  | ATCTGCCTTA | 2100 |
| CCAAGTGTTT | TCTTACTATA  | ATGCTGAATG  | ACTGGAAGAA | AGAAGTGATA  | TGGCTAGTTC | 2160 |
| AGCTAGCTGG | TACAGATAAT  | TCAAAACTGC  | TGTTGGTTTT | AATTTTGTA   | CCTGTGGCCT | 2220 |
| GATCTGTAAA | TAAAACCTTAC | ATTTTTCAAT  | AGGAAAAAAA | AAAAA       | A          | 2271 |

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

|            |            |            |            |            |     |            |            |            |           |            |            |            |            |           |           |
|------------|------------|------------|------------|------------|-----|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|-----------|
| Met<br>1   | Ser        | Phe        | Arg        | Lys<br>5   | Val | Asn        | Ile        | Ile        | Ile<br>10 | Leu        | Val        | Leu        | Ala        | Val<br>15 | Ala       |
| Leu        | Phe        | Leu        | Leu<br>20  | Val        | Leu | His        | His        | Asn<br>25  | Phe       | Leu        | Ser        | Leu        | Ser<br>30  | Ser       | Leu       |
| Leu        | Arg        | Asn<br>35  | Glu        | Val        | Thr | Asp        | Ser<br>40  | Gly        | Ile       | Val        | Gly        | Pro<br>45  | Gln        | Pro       | Ile       |
| Asp        | Phe<br>50  | Val        | Pro        | Asn        | Ala | Leu<br>55  | Arg        | His        | Ala       | Val        | Asp<br>60  | Gly        | Arg        | Gln       | Glu       |
| Glu<br>65  | Ile        | Pro        | Val        | Val<br>70  | Ile | Ala        | Ala        | Ser        | Glu       | Asp<br>75  | Arg        | Leu        | Gly        | Gly       | Ala<br>80 |
| Ile        | Ala        | Ala        | Ile        | Asn<br>85  | Ser | Ile        | Gln        | His        | Asn<br>90 | Thr        | Arg        | Ser        | Asn        | Val<br>95 | Ile       |
| Phe        | Tyr        | Ile        | Val<br>100 | Thr        | Leu | Asn        | Asn        | Thr<br>105 | Ala       | Asp        | His        | Leu        | Arg<br>110 | Ser       | Trp       |
| Leu        | Asn        | Ser<br>115 | Asp        | Ser        | Leu | Lys        | Ser<br>120 | Ile        | Arg       | Tyr        | Lys        | Ile<br>125 | Val        | Asn       | Phe       |
| Asp        | Pro<br>130 | Lys        | Leu        | Leu        | Glu | Gly<br>135 | Lys        | Val        | Lys       | Glu        | Asp<br>140 | Pro        | Asp        | Gln       | Gly       |
| Glu<br>145 | Ser        | Met        | Lys        | Pro<br>150 | Val | Ile        | Phe        | Leu        | Pro       | Phe<br>155 | Thr        | Ile        | Gln        | His       |           |

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```
GCCGACCGAA GAGGCTGGAC ATGACACCAG TGGCATATCA CGGCCATGGG GTCTCAGCAT 60
TCCGCTGCTG CTCGCCCCCTC CTCCTGCAGG CGAAAGCAAG AAGATGACAG GGACGGTTTG 120
CTGGCTGAAC GAGAGCAGGA AGAAGCCATT GCTCAGTTCC CATATGTGGA ATTCACCGGG 180
AGAGATAGCA TCACCTGTCT CACGTGCCAG GGGACAGGCT ACATTCCAAC AGAGCAAGTA 240
AATGAGTTGG TGGCTTTGAT CCCACACAGT GATCAGAGAT TGCGCCCTCA GCGAACTAAG 300
CAATATGTCC TCCTGTCCAT CCTGCTTTGT CTCCTGGCAT CTGGTTTGGT GGTTCCTTC 360
CTGTTTCCGC ATTCAGTCCT TGTGGATGAT GACGGCATCA AAGTGGTGAA AGTCACATTT 420
AATAAGCAAG ACTCCCTTGT AATTCTCACC ATCATGGCCA CCCTGAAAAT CAGGAACTCC 480
AATTCTACA CCGTGGCAGT GACCAGCCTG TCCAGCCAGA TTCAGTACAT GAACACAGTG 540
GTGAATTTTA CCGGGAAGGC CGAGATGGGA GGACCGTTTT CCTATGTGTA CTTCTTCTGC 600
ACGGTACCTG AGATCCTGGT GCACAACATA GTGATCTTCA TGCGAACTTC AGTGAAGATT 660
TCATACATTG GCCTCATGAC CCAGAGCTCC TTGGAGACAC ATCACTATGT GGATTGTGGA 720
GGAAATTCCA CAGCTATTTA ACAACTGCTA TTGGTTCTTC CACACAGCGC CTGTAGAAGA 780
GAGCACAGCA TATGTTCCCA AGGCCTGAGT TCTGGACCTA CCCCCACGTG GTGTAAGCAG 840
AGGAGGAATT GGTTCACCTA ACTCCCAGCA AACATCCTCC TGCCACTTAG GAGGAAACAC 900
CTCCCTATGG TACCATTTAT GTTCTCAGA ACCAGCAGAA TCAGTGCCTA GCCTGTGCC 960
AGCAAATAGT TGGCACTCAA TAAAGATTTG CAGAATTTAA TACAGATCTT TTCAGCTGTT 1020
CTTAGGGCAT TATAAATGGA AATCATAACG TGGTTCTAGG TTATCAAACC ATGGAGTGAT 1080
GTGGAGCTAG GATTGTGAGT GACCTGCAGG CCATTATCAG TGCCTCATCT GTGCAGAAGT 1140
GGCAGCAGAG AGGGACCATC CAAATACCTA AGAGAAAACA GACCTAGTCA GGATATGAAT 1200
TTGTTTCAGC TGTTCCCAAA GGCCTGGGAG CTTTTTGAAG AGAAAGAAAA AAGTGTGTTG 1260
GCTTTTTTTT TTTTGTAGAA GTTAGAATTG TTTTACCAA GAGTCTATGT GGGGCTTGAT 1320
TCACCCTTCA TCCATTGGCT GGAACATGGA TTGGGGATTT GATAGAAAAA TAAACCCTGC 1380
TTTTGATTCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA 1425
```

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```
Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg
 1 5 10 15

Lys Gln Glu Asp Asp Arg Asp Gly Leu Leu Ala Glu Arg Glu Gln Glu
 20 25 30

Glu Ala Ile Ala Gln Phe Pro Tyr Val Glu Phe Thr Gly Arg Asp Ser
 35 40 45

Ile Thr Cys Leu Thr Cys Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln
 50 55 60
```

Val Asn Glu Leu Val Ala Leu Ile Pro His Ser Asp Gln Arg Leu Arg  
65 70 75 80

Pro Gln Arg Thr Lys Gln Tyr Val Leu Leu Ser Ile Leu Leu Cys Leu  
85 90 95

Leu Ala Ser Gly Leu Val Val Phe Phe Leu Phe Pro His Ser Val Leu  
100 105 110

Val Asp Asp Asp Gly Ile Lys Val Val Lys Val Thr Phe Asn Lys Gln  
115 120 125

Asp Ser Leu Val Ile Leu Thr Ile Met Ala Thr Leu Lys Ile Arg Asn  
130 135 140

Ser Asn Phe Tyr Thr Val Ala Val Thr Ser Leu Ser Ser Gln Ile Gln  
145 150 155 160

Tyr Met Asn Thr Val Val Asn Phe Thr Gly Lys Ala Glu Met Gly Gly  
165 170 175

Pro Phe Ser Tyr Val Tyr Phe Phe Cys Thr Val Pro Glu Ile Leu Val  
180 185 190

His Asn Ile Val Ile Phe Met Arg Thr Ser Val Lys Ile Ser Tyr Ile  
195 200 205

Gly Leu Met Thr Gln Ser Ser Leu Glu Thr His His Tyr Val Asp Cys  
210 215 220

Gly Gly Asn Ser Thr Ala Ile  
225 230

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CTTCCAAAGA GCGACTCTTA CTGTTTCTCA TGGTGAGAAG ACAATATTTG CTTTCTCTTT | 60  |
| TTCCTTTCTT CCGGATGAGA GGCTAAGCCA TAATAGAAAG AATGGAGAAT TATTGATTGA | 120 |
| CCGTCTTTAT TCTGTGGGCT CTGATTCTCC AATGGGAATA CCAAGGGATG GTTTTCCATA | 180 |
| CTGGAACCCA AAGGTAAAGA CACTCAAAGA CAGACATTTT TGGCAGAGCA TAGATGAAAA | 240 |
| TGGCAAGTTC CCTGGCTTTC CTTCTGCTCA ACTTTCATGT CTCCCTCCTC TTGGTCCAGC | 300 |
| TGCTCACTCC TTGCTCAGCT CAGTTTTCTG TGCTTGGACC CTCTGGGCCC ATCCTGGCCA | 360 |
| TGGTGGGTGA AGACGCTGAT CTGCCCTGTC ACCTGTTCCC GACCATGAGT GCAGAGACCA | 420 |
| TGGAGCTGAA GTGGGTAAGT TCCAGCCTAA GGCAGGTGGT GAATGTGTAT GCAGATGGAA | 480 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| AGGAAGTGA AGACAGGCAG AGTGCACCGT ATCGAGGGAG AACTTCGATT CTGCGGGATG  | 540  |
| GCATCACTGC AGGGAAGGCT GCTCTCCGAA TACACAACGT CACAGCCTCT GACAGTGGAA | 600  |
| AGTACTTGTG TTATTTCCAA GATGGTGA CTCTATGAAAA AGCCCTGGTG GAGCTGAAGG  | 660  |
| TTGCAGCACT GGGTTCTAAT CTCACGTCG AAGTGAAGGG TTATGAGGAT GGAGGGATCC  | 720  |
| ACCTGGAGTG CAGGTCCACC GGCTGGTACC CCCAACCCCA AATACAGTGG AGCAACGCCA | 780  |
| AGGGAGAGAA CATCCCAGCT GTGGAAGCAC CTGTGGTTGC AGACGGAGTG GGCCTATATG | 840  |
| AAGTAGCAGC ATCTGTGATC ATGAAAGGCG GCTCCGGGGA GGGTGTATCC TGCATCATCA | 900  |
| GAAATTCCCT CCTCGGCCTG GAAAAGACAG CCAGCATTTT CATCGCAGAC CCCTTCTTCA | 960  |
| GGAGCGCCCA GCCCTGGATC GCAGCCCTGG CAGGGACCCT GCCTATCTTG CTGCTGCTTC | 1020 |
| TCGCCGGAGC CAGTTACTTC TTGTGGAGAC TACAGAAGGA AATAACTGCT CTGTCCAGTG | 1080 |
| AGATAGAAAG TGAGCAAGAG ATGAAAGAAA TGGGATATGC TGCAACAGAG CGGGAAATAA | 1140 |
| GCCTAAGAGA GAGCCTCCAG GAGGAACTCA AGAGGAAAAA AATCCAGTAC TTGACTCGTG | 1200 |
| GAGAGGAGTC TTCGTCCGAT ACCAATAAGT CAGCCTGATG CTCTAATGGA AAAATGGCCC | 1260 |
| TCTTCAAGCC TGCCTGATTT TTCCTGCATG GGAAGAGCGC ACATGTNGCC CTGAGGTTCC | 1320 |
| CTTCCCAGGA CNGCTCCAGG ATCGAGATCA CTGTGAGTGG TTGTGGAGTT AAGACCCCTA | 1380 |
| TGGACTCCTT CCCAGCTGAT TATCAGAGCC TTAGACCCAG CACTCCTTGG ATTGGCTCTG | 1440 |
| CAGAGTGTCT TGGTTGAGAG AATAACGTTG CAGTTCCAC AGGGCATGTG ACTTTGAAAG  | 1500 |
| AGACTAAAGG CCACACTCTG TTAATAATGG GGCACATATG TGTTCCACC CCACAAATGT  | 1560 |
| GATAAGTGAT CGTGCAGCCA GAGCCAGCCT TCCTTCAGTC AAGGTTTCCA GGCAGAGCAA | 1620 |
| ATACCCTAGA GATTCTCTGT AATATTGGTA ATTTGGATGA AGGAAGCTAG AAGAATTACA | 1680 |
| GGGATGTTTT TAATCCCACT ATGGACTCAG TCTCCTGGAA AAGGATCTGT CCACTCCTGG | 1740 |
| TCATTGGTGG ATGTTAAACC CATATTCCTT TCAACTGCTG CCTGCTAGGG AAAACTGCTC | 1800 |
| CTCATTATCA TCACTATTAT TGCTCACCAC TGTATCCCCT CTACTGGGCA AGTGCTTGTC | 1860 |
| AAGTTCTAGT TGTTCAATAA ATTTGTTAAT AATGCTGAAA AAAAAAAAAA AAAAAAAAAA | 1920 |
| A                                                                 | 1921 |

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Lys Met Ala Ser Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val  
1 5 10 15

Ser Leu Leu Leu Val Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser  
20 25 30

Val Leu Gly Pro Ser Gly Pro Ile Leu Ala Met Val Gly Glu Asp Ala  
35 40 45

Asp Leu Pro Cys His Leu Phe Pro Thr Met Ser Ala Glu Thr Met Glu  
50 55 60

Leu Lys Trp Val Ser Ser Ser Leu Arg Gln Val Val Asn Val Tyr Ala  
65 70 75 80

Asp Gly Lys Glu Val Glu Asp Arg Gln Ser Ala Pro Tyr Arg Gly Arg  
85 90 95

Thr Ser Ile Leu Arg Asp Gly Ile Thr Ala Gly Lys Ala Ala Leu Arg  
100 105 110

Ile His Asn Val Thr Ala Ser Asp Ser Gly Lys Tyr Leu Cys Tyr Phe  
115 120 125

Gln Asp Gly Asp Phe Tyr Glu Lys Ala Leu Val Glu Leu Lys Val Ala  
130 135 140

Ala Leu Gly Ser Asn Leu His Val Glu Val Lys Gly Tyr Glu Asp Gly  
145 150 155 160

Gly Ile His Leu Glu Cys Arg Ser Thr Gly Trp Tyr Pro Gln Pro Gln  
165 170 175

Ile Gln Trp Ser Asn Ala Lys Gly Glu Asn Ile Pro Ala Val Glu Ala  
180 185 190

Pro Val Val Ala Asp Gly Val Gly Leu Tyr Glu Val Ala Ala Ser Val  
195 200 205

Ile Met Lys Gly Gly Ser Gly Glu Gly Val Ser Cys Ile Ile Arg Asn  
210 215 220

Ser Leu Leu Gly Leu Glu Lys Thr Ala Ser Ile Ser Ile Ala Asp Pro  
225 230 235 240

Phe Phe Arg Ser Ala Gln Pro Trp Ile Ala Ala Leu Ala Gly Thr Leu  
245 250 255

Pro Ile Leu Leu Leu Leu Ala Gly Ala Ser Tyr Phe Leu Trp Arg  
260 265 270

Leu Gln Lys Glu Ile Thr Ala Leu Ser Ser Glu Ile Glu Ser Glu Gln  
275 280 285

Glu Met Lys Glu Met Gly Tyr Ala Ala Thr Glu Arg Glu Ile Ser Leu  
290 295 300

Arg Glu Ser Leu Gln Glu Glu Leu Lys Arg Lys Lys Ile Gln Tyr Leu  
305 310 315 320



Thr Arg Gly Glu Glu Ser Ser Ser Asp Thr Asn Lys Ser Ala  
325 330

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

```
AATGGTTCCA GCCTTAATGG AGAAGCCAGT TTCTTTTTTC TTGTTGTTTT ATTGTTTTTA 60
AGCCTCTCTC TGGTTTTTCAG TAGAGTTTGA CCTTAAATAT CATCTTTGAT TACTATTGGT 120
GTCCTTGTAG TTAAGGTCTT TGCAAAAGTT TGAGTGCAAG TTTTAAGCTA AAAACACGTT 180
TTTAAACTTT CACAAATTTT GTAAGATGAC AATAGCATTC TGTAACATAG ACATTATGGT 240
AATAGTGATT TTCTCTCCAT CCCTATTTTG TCCAGCGATT TCCAAGTTAT AAGACGTGAA 300
TAAGACTAAC CGCTCACTTC CACCAGCAGC TGACCTGGTG GGCTTTTGAG TTCAAAGAGT 360
CATTTCTTCA TCTTACCTCC AGCACTGCAG GGCCGTGTGA CCTTGCAGAG CCTTGTCTTCT 420
CATTGATGAA AGGAGCTCAT GCCTCATGAA GCCACTGGTA AGGGCCATGG AGCTCACGGG 480
CCATCAAGCT TCCTTCCCAT CACTTGTGGG TGGAAATTGAC ATTACCCGAT GAGCTCTTCC 540
TGGGGTCACC TGGGAGGGAG TGGCCCATGG GTGGATGAC AAAATCTCAT AGTCAGTCTT 600
TGCAGTTTTT TCCACAGGTA AAATGAGATT TTGGAAAATT TTCATTGTGT TGTATTGTGTC 660
CCAAGGTGAG TCTTACATAT TTTGAGCAAC AAAACGAAGA TCATTATGAA AATGTCCTTA 720
TGGAAGCACT CTAGGGCCAT TGCTCATTTT TATGAGTCCT CGTGCTAAGT CCCTGAGTAC 780
TGTGGCTCAT GTCTTAGCTG GCTAAATCAC AGTCAAAATT CTCTTCTTAA GCCTCAAAAT 840
AAGCTGCTGA TTATACTGCC TGTTGGCCAG ACTAATCAAA TACATTTGAT GTTTTAGCTG 900
ACTCCAGATA CTTTTCTTTC CTCCTCCTTG GTTCTTTAAC TGTCATCCCA GATCTGCGAC 960
ATGCAATAAG GAAAACAGAG TCAGGGAGGA AGTAGGATTC CTTTGTCTGC TAGGAACCAC 1020
GTTAGCTTTG GATTGTCCAT AGAATGCACC CTTAACAGTT CTTGGAAAAT GGATGATATT 1080
TGGTTCCTGC CCCATGTTCA GTGTTCTTTG GCAGCTGCAA AGCATATCCT AGCTAGAATC 1140
CTTATCGTCT TGAAGTTCAT CAAAGATTTT GAACAGTCAT GGTGGAGATA CAACCTAAGT 1200
ACATTCATGC CCATTGAGAC AATCCTTTGG TTTGAGCGAC GGAAGGAGGA ATAAACACAT 1260
GAATGTATTT TATTGAATCC CAGAGACCCT GAAACACCAA GACTCATTAA TATATGCATA 1320
CATGGATGGC AGAATAATAA ACCTCACCTG ACCTGTCAGT GTACTCTCAG TTTTAAAGGT 1380
TCTCCCAAAA CAGGGAAACT GAAAAATACT TGGGCAGAAA GAAAATATCA TCAAATAACA 1440
CCTATTTCTT TTCAGCTATA GAGATGGCTG GATATCAAAA GCACCACGGG AGCTTTGCAA 1500
TTTGCTGCTC TTTTCAGCCC TCAGCTTGAC TCTCAGTTT CAAGAGGGAG AAAATGAATG 1560
TTTCCCAGCA TTCTCTGTCC TTTGCTCCAA AGAAGAGAGC AGGTGTTGGC TTCCAAACCT 1620
TCCGTATTTT CTTATTGCTG TTAGGGGGAT CAACTGCATG TTTCTTGAGG GAAAAGGGTG 1680
GCTCACTGAC CTAATTGAAG GCATTCTCTC AGTGAAGCT GGGCAAGAGA ATCCAGGGAT 1740
TTCTTTTGCA GGTTCCTGCG CAGTGCCCTT GCCATCAAGC TGCCTAAAAT GTGAATATTG 1800
CTTCCCTGCG TTTCAAGAGT GGTAAATATT GGGCAAGTGG TGGAGGATCT AAAAAAAAAA 1860
AAAAA 1865
```

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met Asn Val Ser Gln His Ser Leu Ser Phe Ala Pro Lys Lys Arg Ala

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2094 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

-106-

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

Met Ser Ala Arg Thr Gln Phe Ile Cys Leu Ile Gly Phe Ile Lys Leu
 1 5 10 15
Leu Glu Asn Phe Ser Ile Cys Tyr Phe Phe Pro Leu His Leu Leu Ser
 20 25 30
Asn Ala Pro Asn Glu Phe Val Thr Gln Ser Gln Leu Phe Pro Ser Leu
 35 40 45
Ser His Cys Phe Leu Leu Ser Pro Thr His Arg Ile Asn Met Lys Leu
 50 55 60
Ser Ser Arg Ser Val Met Ile Ser Leu Arg Lys Asn Phe
 65 70 75

```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2069 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```

AAATTCAACA TAAACCCAAA TCTGTACTTC TCCAGAGGAG CAGCTCTGAG GTAGAAATTA 60
CAACGATGAA AAGAGCACAA CGTACAAAAC CAAGAAAGAG TCTGTTGTGT GAAGGGTCAT 120
TCGATGAAGA AGCTTCTGCA CAGTCCTTTC AGGAAGTGTT AAGTCAATGG AGAACCGGAA 180
ATCATGATGA CAACAAGAAA CAGAATTTAC ATGCAGCAGT AAAAGACTCA TTGGAAGAAT 240
GCGAAGTACA GACTAATCTG AAAATTTGGA GAGAACCACT TAATATTGAA CTTAAAGAAG 300
ACATTCTATC CTATATGGAA AAATTATGGC TTAAAAACA CAGGAGAACT CCACAAGAGC 360
AACTTTTTAA AATGCTACCA GATACGTTCC CACATCCACA TGAAACCACT GGTGATGCAC 420
AGTGTTCTCA AAATGAAAAC GATGAAGATA GTGATGGTGA GGAGACCAA GTACAACACA 480
CAGCTCTTTT ATTGCCAGTA GAAACATTAA ACATAGAGAG ACCTGAACCA TCTCTAAAGA 540
TAGTCGAACCT GGATGATACT TATGAAGAGG AATTTGAAGA AGCAGAAAAT ATTGTGCCTT 600
ACAAAGTTAA ATTAGCTGAT GCAGACAGTC AACGAAGTTG TGCTTTTCAT GATTGTCAGA 660
AGAATAGCTT TCCATATGAA AATGGCATCC ATCAACATCA TGTTTTCGAT AAGGGAAAAG 720
GAGACTTCTT AAATCTTTGT CTGAGAAACA GCTATACTTA TTATAAAGAT AATTCAAAAG 780
CAGAACTTTC AAACACAGAT TTTGACAACA TCGTGGATCC TGATGTGTAT TCTTCTGACA 840
TTGAAAAAAT TGAGGAAAGC ACCTCCTTTG AAAGAAATTT AAAGGAGAAA AATATAGGTT 900
TAGAAAGTAA TCAAAAGTCT GATGATTCCT GTGTATCACT TGAAAGCAAG GACACTTTGC 960
TAGGTAGAGA TTTAGAAAAA GCTCCCATTG AGGAGAAATT ATCTCAAGAC ATCAAAGAAT 1020
CCTTGGAATT GAGCAATCTG TATAAGAGGC CAAGCTTTGA AGAATCAAAA ACTACAAAGT 1080
CATCACTGTT GTTACAAGAA ATAGCCTGCA GAAGTAAGCC TATAACAAAA CAATATCAAG 1140
GACTTGAGAG ATTCTTTATT TTTGATACAA ATGAAAGACT CAACTTACTT CCTTCTCATC 1200
GTTTAGAATG CAACAATTCC AGTACTAGGA TTACACTTGC AGAAGACAGA GAATGGATTTC 1260

```

CAGACCATAG CTTAAGTGAA TATGCTGATA ATGCAATTGT CTTGGGTGTT CTGCAGGGTG 1320  
 CTCAGAGTCC ATCATCAAGT AGAAAACAGC AAAAGATGGG TCAGAAATCA CAGAGACCTT 1380  
 CAACAGCAAA TTTTCCACTT TCCAACCTCTG TTAAGAAAG CTCCAGTTGC CTTTCATCCT 1440  
 CTCATCCTCG ATCAAGAAGT GCAGCTGCTC AATCATCATC TAGAGCTGCT TCTGAAATTT 1500  
 CAGAAATTGA ATATATTGAT ATTACTGACC AGAATGAGCT TTCCTTAGAT GACACTACTG 1560  
 ATCAACATAC TTTAGACAAAT TTGGAAAAAG AATTACAAGT GCTGAGATCT CTTGCAGATA 1620  
 CTTCAGAAAA GCTTTACAGC TTAACCTCAG AAGAGTTCCC AGATTTCAGC AGCCAATCAC 1680  
 TGAATATAAG TCAGATTTCC ACAGATTTCC TTAAGACCTC ACATGTGAGG GGTCCCTGTG 1740  
 GAGTTGAGGA ATTGAGCTGT TCTGGAAGAG ATACCAAAT TCAGTCTTTG CTGTCACTTT 1800  
 CTGAGAGCAG TACAGATGAG GAGGAGGAAG ATTTTCTCAA CAAGCAACAT GTCATCACAC 1860  
 TACCGTGGTC AAAGAGTACT TAAAGATTAT TTGTTCATTA CTGTTTCCAT TTTGTACCCA 1920  
 GAGTAAAGCA AACAACAGT AAAAGTAACC AAGTGATTAC CTATCCAAGT GCTGGAGATT 1980  
 TTGATTACTA ATGTCTTTGA TGTTTCAAGG CTACAAACTA ATAAAAGTAA AATTATAAGT 2040  
 TCAAAAAAAA AAAAAAAA AAAAAAAA 2069

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met Lys Arg Ala Gln Arg Thr Lys Pro Arg Lys Ser Leu Leu Cys Glu  
 1 5 10 15  
 Gly Ser Phe Asp Glu Glu Ala Ser Ala Gln Ser Phe Gln Glu Val Leu  
 20 25 30  
 Ser Gln Trp Arg Thr Gly Asn His Asp Asp Asn Lys Lys Gln Asn Leu  
 35 40 45  
 His Ala Ala Val Lys Asp Ser Leu Glu Glu Cys Glu Val Gln Thr Asn  
 50 55 60  
 Leu Lys Ile Trp Arg Glu Pro Leu Asn Ile Glu Leu Lys Glu Asp Ile  
 65 70 75 80  
 Leu Ser Tyr Met Glu Lys Leu Trp Leu Lys Lys His Arg Arg Thr Pro  
 85 90 95  
 Gln Glu Gln Leu Phe Lys Met Leu Pro Asp Thr Phe Pro His Pro His  
 100 105 110  
 Glu Thr Thr Gly Asp Ala Gln Cys Ser Gln Asn Glu Asn Asp Glu Asp  
 115 120 125  
 Ser Asp Gly Glu Glu Thr Lys Val Gln His Thr Ala Leu Leu Leu Pro  
 130 135 140  
 Val Glu Thr Leu Asn Ile Glu Arg Pro Glu Pro Ser Leu Lys Ile Val  
 145 150 155 160  
 Glu Leu Asp Asp Thr Tyr Glu Glu Glu Phe Glu Glu Ala Glu Asn Ile  
 165 170 175  
 Val Pro Tyr Lys Val Lys Leu Ala Asp Ala Asp Ser Gln Arg Ser Cys

|                                                                                    |     |     |
|------------------------------------------------------------------------------------|-----|-----|
| 180                                                                                | 185 | 190 |
| Ala Phe His Asp Cys Gln Lys Asn Ser Phe Pro Tyr Glu Asn Gly Ile<br>195 200 205     |     |     |
| His Gln His His Val Phe Asp Lys Gly Lys Arg Asp Phe Leu Asn Leu<br>210 215 220     |     |     |
| Cys Leu Arg Asn Ser Tyr Thr Tyr Tyr Lys Asp Asn Ser Lys Ala Glu<br>225 230 235 240 |     |     |
| Thr Ser Asn Thr Asp Phe Asp Asn Ile Val Asp Pro Asp Val Tyr Ser<br>245 250 255     |     |     |
| Ser Asp Ile Glu Lys Ile Glu Glu Ser Thr Ser Phe Glu Arg Asn Leu<br>260 265 270     |     |     |
| Lys Glu Lys Asn Ile Gly Leu Glu Ser Asn Gln Lys Ser Asp Asp Ser<br>275 280 285     |     |     |
| Cys Val Ser Leu Glu Ser Lys Asp Thr Leu Leu Gly Arg Asp Leu Glu<br>290 295 300     |     |     |
| Lys Ala Pro Ile Glu Glu Lys Leu Ser Gln Asp Ile Lys Glu Ser Leu<br>305 310 315 320 |     |     |
| Glu Leu Ser Asn Leu Tyr Lys Arg Pro Ser Phe Glu Glu Ser Lys Thr<br>325 330 335     |     |     |
| Thr Lys Ser Ser Leu Leu Leu Gln Glu Ile Ala Cys Arg Ser Lys Pro<br>340 345 350     |     |     |
| Ile Thr Lys Gln Tyr Gln Gly Leu Glu Arg Phe Phe Ile Phe Asp Thr<br>355 360 365     |     |     |
| Asn Glu Arg Leu Asn Leu Leu Pro Ser His Arg Leu Glu Cys Asn Asn<br>370 375 380     |     |     |
| Ser Ser Thr Arg Ile Thr Leu Ala Glu Asp Arg Glu Trp Ile Pro Asp<br>385 390 395 400 |     |     |
| His Ser Leu Ser Glu Tyr Ala Asp Asn Ala Ile Val Leu Gly Val Leu<br>405 410 415     |     |     |
| Gln Gly Ala Gln Ser Pro Ser Ser Ser Arg Lys Gln Gln Lys Met Gly<br>420 425 430     |     |     |
| Gln Lys Ser Gln Arg Pro Ser Thr Ala Asn Phe Pro Leu Ser Asn Ser<br>435 440 445     |     |     |
| Val Lys Glu Ser Ser Ser Cys Leu Ser Ser Ser His Pro Arg Ser Arg<br>450 455 460     |     |     |
| Ser Ala Ala Ala Gln Ser Ser Ser Arg Ala Ala Ser Glu Ile Ser Glu<br>465 470 475 480 |     |     |
| Ile Glu Tyr Ile Asp Ile Thr Asp Gln Asn Glu Leu Ser Leu Asp Asp<br>485 490 495     |     |     |
| Thr Thr Asp Gln His Thr Leu Asp Asn Leu Glu Lys Glu Leu Gln Val<br>500 505 510     |     |     |

Leu Arg Ser Leu Ala Asp Thr Ser Glu Lys Leu Tyr Ser Leu Thr Ser  
515 520 525

Glu Glu Phe Pro Asp Phe Ser Ser Gln Ser Leu Asn Ile Ser Gln Ile  
530 535 540

Ser Thr Asp Phe Leu Lys Thr Ser His Val Arg Gly Pro Cys Gly Val  
545 550 555 560

Glu Glu Leu Ser Cys Ser Gly Arg Asp Thr Lys Ile Gln Ser Leu Leu  
565 570 575

Ser Leu Ser Glu Ser Ser Thr Asp Glu Glu Glu Glu Asp Phe Leu Asn  
580 585 590

Lys Gln His Val Ile Thr Leu Pro Trp Ser Lys Ser Thr  
595 600 605

## (2) INFORMATION FOR SEQ ID NO:141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```

GTCCTGGATG GCGGAGCCTT GGGTTCCGGG GGCCTGGGAC CTGCAACTCT TTCTACAAGA 60
TATCAAGTTA TTCTAGTACA ACCATATAAA TAAATAATAC CTGAAGTCTC AGTGTAACAT 120
GGACAATTAA CAGTGATGAC AGATAAATAC AGACGCATGG GGATCAAATA CTAGGCAAAA 180
CGCTTTTAA AAGTGATCA GGCTTTTAAG AAACACTGCA GGATCCTGTC TATCTTAATG 240
CTGATAGAGC TCAGCTAAAA ATTTAGGAGG TTCTAGTATT CTTTATGGCT GAAGCTGAGA 300
GAGTCTGAAA CCCTGATGCT TAAGCTCCAT TCTAGATCAT AGCTCCAACCT CCTTCAGGAT 360
ATAAGGAAAA GAGATTATAT TTCCACAATG ATAGATCTTT GGTGTGACAG GTTTCCCAAT 420
GAGTGGATCA TGATGACCGT ATTGTAGGGA CTGCGCATAG TATGGCTGCT TCCCGATCTA 480
CTCGTGTTAC MAGATCAACA GTGGGGTTAA ACGGCTTGGA TGAATCTTTT TGTGGTAGAA 540
CTTTAAGGAA TCGTAGCATT GCGCATCCTG AAGAAATCTC TTCTAATTCT CAAGTACGAT 600
CAAGATCACC AAAGAAGAGA CCAGAGCCTG TGCCAATTCA GAAAGGAAAT AATAATGGGA 660
GAACCACTGA TTTAAAAAG CAGAGTACCC GAGAATCATG GGTAAGCCCT AGGAAAAGAG 720
GACTTTCTTC TTCAGAAAAG GATAACATAG AAAGGCAGGC TATAGAAAAT TGTGAGAGAA 780
GGCAAACAGA ACCTGTTTCA CCAGTTTTAA AAAGAATTAA GCGTTGTCTT AGATCTGAAG 840
CACCAAACAG TTCAGAAGAA GATTCTCCTA TAAAATCAGA CAAGGAGTCA GTAGAACAGA 900
GGAGTACAGT AGTGGACAAT GATGCAGATT TTCAAGGGAC TAAACGAGCT TGTCGATGTC 960
TTTACTGGA TGATTGTGAG AAAAGGGAAA TTTAAAAGGT GAATGTCAGT GAGGAAGGGC 1020
CACTTAATTC TGCAGTAGTT GAAGAAATCA CAGGCTATTT GGCTGTCAAT GGTGTTGATG 1080
ACAGTGATT AGCTGTTATA AACTGTGATG ACTGTCAGCC TGATGGGAAC ACTAAACAAA 1140
ATAGCATTTG TTCTATGTG TTACAGGAAA AATCAGTAGC TGAAAATGGG GATACGGATA 1200
CCCAAACCTT AATGTTCTT GATAGTAGGA AGGAGGACAG TTATATAGAC CATAAGGTGC 1260
CTTGACACAGA TTCACAAGTG CAGGTCAAGT TGGAGGACCA CAAAATAGTA ACTGCCTGCT 1320
TGCCTGTGGA ACATGTTAAT CAGCTGACTA CTGAGCCAGC TACAGGGCCC TTTTCTGAAA 1380
CTCAGTCATC TTTAAGGGAT TCTGAGGAGG AAGTAGATGT GGTGGGAGAT AGCAGTGCCT 1440
CAAAAGAGCA GTGTAAAGAA AACACCAATA ACGAACTGGA CACAAGTCTT GAGAGTATGC 1500
CAGCCTCCGG AGAACCTGAA CCATCTCCTG TTCTAGACTG TGTATCAGCT CAAATGATGT 1560
CTTTATCAGA ACCTCAAGAA CATCGTTATA CTCTGAGAAC CTCACCACGA AGGGCAGCCC 1620
CTACCAGAGG TAGTCCCCT AAAAACAGTT CTCCTTACAG AGAAAATGGA CAATTTGAGG 1680
AGAATAATCT TAGTCCTAAT GAAACAAATG CAACGTGTAG TGATAATGTA AGTCAATCTC 1740
CTACAAATCC TGGTGAAATT TCTCAAATG AAAAAGGGAT ATGTTGTGAC TCTCAAATA 1800

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ATGGAAGTGA AGGAGTAAGT AAACCACCCCT CAGAGGCAAG ACTCAATATT GGACATTTGC 1860
CATCTGCCAA AGAGAGTGCC AGTCAGCACA TTACAGAAGA GGAAGATGAT GATCCTGATG 1920
TTTATTACTT TGAATCAGAT CATGTGGCAC TGA AACACAA CAAAGATTAT CAGAGACTAT 1980
TACAGACGAT TGCTGTACTC GAGGCTCAGC GTTCTCAAGC AGTCCAAGAC CTTGAAAGTT 2040
TAGGCAGGCA CCAGAGAGAA GCACTGAAAA ATCCCATTGG ATTTGTGGAA AACTCCAGA 2100
AGAAGGCTGA TATTGGGCTT CCATATCCAC AGAGAGTTGT TCAATTGCCT GAGATCGTAT 2160
GGGACCAATA TACCCATAGC CTTGGGAATT TTGAAAGAGA ATTTAAAAAT CGTAAAAGAC 2220
ATACTAGAAG AGTTAAGCTA GTTTTTGATA AAGTAGGTTT ACCTGCTAGA CAAAAAGTC 2280
CTTTAGATCC TAAGAAGGAT GGAGAGTCCC TTTTCATATC TATGTTGCCT TTGAGTGATG 2340
GTCCAGAAGG CTCAAGCAGT CGTCCTCAGA TGATAAGAGG ACGCTTGTGT GATGATACCA 2400
AACCTGAAAC ATTTAACCAG TTGTGGACTG TTGAAGAACA GAAAAAGCTG GAACAGCTAC 2460
TCATCAAATA CCCTCCTGAA GAAGTAGAAT CTCGACGCTG GCAGAAGATA GCAGATGAAT 2520
TGGGCAACAG GACAGCAAAA CAGGTTGCCA GCCGAGTACA GAAGTATTTT ATAAAGCTAA 2580
CTAAAGCTGG CATTCCAGTA CCAGGCAGAA CACCAAACCT ATATATATAC TCCAAAAAGT 2640
CTTCAACAAG CAGACGACAG CACCCTCTTA ATAAGCATCT CTTAAGCCT TCCACTTTCA 2700
TGACTTCACA TGAACGCCCA GTGTATATGG ATGAAGATGA TGACCGATCT TGTTCATATA 2760
GCCACATGAA CACTGCTGTT GAAGATGCAT CAGATGACGA AAGTATTCCT ATCATGTATA 2820
GGAATTTACC TGAATATAAA GAACTATTAC AGTTTAAAAA GTTAAAGAAG CAGAACTTC 2880
AGCAAATGCA AGCTGAAAGT GGATTTGTGC AACATGTGGG CTTAAGTGT GATAACTGTG 2940
GCATAGAACC CATCCAGGGT GTTCGGTGGC ATTGCCAGGA TTGTCCTCCA GAAATGTCTT 3000
TGGATTTCTG TGATTCCTGT TCAGACTGTC TACATGAAAC AGATATTCAC AAGGAAGATC 3060
ACCAATTAGA ACCTATTTAT AGGTCAGAGA CATTCTTAGA CAGAGACTAC TGTGTGTCTC 3120
AGGGCACCAG TTACAATTAC CTTGACCCAA ACTACTTTCC AGCAAAACAGA TGACATGGAA 3180
GAGAACATCA TTTACTAGTC CTCTTCAACA CATAGCAATG GTATCATTGT TAATTATGTG 3240
CACAGTTTGG AAAGATTCTC TGCTTTCCCA GAAATGACAC TCACAGCATG AGAGCTTCCT 3300
GAGTGTTCTC GTCAAGTACA GCTCTGCACC GTTGTGGCTC TAGATCACTG TTCAGCAGCT 3360
GAACATTCCT GGTGAGCAAA GGTTTCCCTG GTGAATTTTT CACCACTGCG TTTTAGGTGG 3420
TGATCTTAAA TGGGTGAGAT GGAACGAGAG CACACATTAA AGAGAGAGTA AATTCCAAAG 3480
GTTTCAAAGA ACTTGGTCAT AAATATGATA ATGAGAAGAC AAAGTATTTA TATTAAAACA 3540
GTTTAGTAGC CTTCAGTTTT GTGAAAATAG TTTTCAGCAC AGAAACTGAC TTCTTTAGAC 3600
AAAGTTTTAA CCAATGATGG TGTTTGCTTC TAGGATATAC ACTTTAAAAG AACTCACTGT 3660
CCCAGTGGTG GTCATFGATG GCCTTTAGTA AATTGGAGCT GCTTAATCAT ATTGATATCT 3720
AATTTCTTTT AACCACAATG AATTGTCCTT AATTACCAAC AGTGAAGCAC TACAGGAGGC 3780
AAGTGTGGCA TTGCTTCCTT AACCAGCTCA TGGTGTGTGA ATGTTATAAA ATTGTCATC 3840
AGATATATTT TTTAAATGTA ATGTTATATA AGATGATCAT GTGATGTGTA CAACTATGG 3900
TGAAAAGTGC CAGTGGTAGT AACTGTGTAA AGTTTCTAAT TCACAACATT AATTCCTTTA 3960
AAATACACAG CCTTCTGCCT CTGTATTTGG AGTTGTCAGT ACAACTCATC AAAGAAAAC 4020
GCCTAATATA AAAATCATAT ATATGGTAAT AATTTCCCTC TTTTGTAGTC TGCACAAGAT 4080
CCATAAAAGA TTGTATTTTT ATTACTATTT AAACAAGTGA TTAAATTTAG TCTGCACAGT 4140
GAGCAAGGGT TCACATGCAT TCTTTTATAC TGCTGGATTT TGTTGTGCAT CATTTAAAAC 4200
ATTTTGTATG TTTCTTCTTA TCTGTGTATA CAGTATGTTT TTGAATGATG TTCATTTGTC 4260
AGGAGAACTG TGAGAAATAA ACTATGTGGA TACTGTCTGT TTMTRTCAAA AAAAAAAAAA 4320
AAAAAAAAA AAAAAAA 4337

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## (2) INFORMATION FOR SEQ ID NO:142:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```

Met Ala Ala Ser Arg Ser Thr Arg Val Thr Arg Ser Thr Val Gly Leu
 1 5 10 15

```

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Asn Gly Leu Asp Glu Ser Phe Cys Gly Arg Thr Leu Arg Asn Arg Ser
 20 25 30

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Ile Ala His Pro Glu Glu Ile Ser Ser Asn Ser Gln Val Arg Ser Arg  
 35 40 45  
 Ser Pro Lys Lys Arg Pro Glu Pro Val Pro Ile Gln Lys Gly Asn Asn  
 50 55 60  
 Asn Gly Arg Thr Thr Asp Leu Lys Gln Gln Ser Thr Arg Glu Ser Trp  
 65 70 75 80  
 Val Ser Pro Arg Lys Arg Gly Leu Ser Ser Ser Glu Lys Asp Asn Ile  
 85 90 95  
 Glu Arg Gln Ala Ile Glu Asn Cys Glu Arg Arg Gln Thr Glu Pro Val  
 100 105 110  
 Ser Pro Val Leu Lys Arg Ile Lys Arg Cys Leu Arg Ser Glu Ala Pro  
 115 120 125  
 Asn Ser Ser Glu Glu Asp Ser Pro Ile Lys Ser Asp Lys Glu Ser Val  
 130 135 140  
 Glu Gln Arg Ser Thr Val Val Asp Asn Asp Ala Asp Phe Gln Gly Thr  
 145 150 155 160  
 Lys Arg Ala Cys Arg Cys Leu Ile Leu Asp Asp Cys Glu Lys Arg Glu  
 165 170 175  
 Ile Lys Lys Val Asn Val Ser Glu Glu Gly Pro Leu Asn Ser Ala Val  
 180 185 190  
 Val Glu Glu Ile Thr Gly Tyr Leu Ala Val Asn Gly Val Asp Asp Ser  
 195 200 205  
 Asp Ser Ala Val Ile Asn Cys Asp Asp Cys Gln Pro Asp Gly Asn Thr  
 210 215 220  
 Lys Gln Asn Ser Ile Gly Ser Tyr Val Leu Gln Glu Lys Ser Val Ala  
 225 230 235 240  
 Glu Asn Gly Asp Thr Asp Thr Gln Thr Ser Met Phe Leu Asp Ser Arg  
 245 250 255  
 Lys Glu Asp Ser Tyr Ile Asp His Lys Val Pro Cys Thr Asp Ser Gln  
 260 265 270  
 Val Gln Val Lys Leu Glu Asp His Lys Ile Val Thr Ala Cys Leu Pro  
 275 280 285  
 Val Glu His Val Asn Gln Leu Thr Thr Glu Pro Ala Thr Gly Pro Phe  
 290 295 300  
 Ser Glu Thr Gln Ser Ser Leu Arg Asp Ser Glu Glu Glu Val Asp Val  
 305 310 315 320  
 Val Gly Asp Ser Ser Ala Ser Lys Glu Gln Cys Lys Glu Asn Thr Asn  
 325 330 335  
 Asn Glu Leu Asp Thr Ser Leu Glu Ser Met Pro Ala Ser Gly Glu Pro  
 340 345 350



Glu Pro Ser Pro Val Leu Asp Cys Val Ser Ala Gln Met Met Ser Leu  
 355 360 365  
 Ser Glu Pro Gln Glu His Arg Tyr Thr Leu Arg Thr Ser Pro Arg Arg  
 370 375 380  
 Ala Ala Pro Thr Arg Gly Ser Pro Thr Lys Asn Ser Ser Pro Tyr Arg  
 385 390 395 400  
 Glu Asn Gly Gln Phe Glu Glu Asn Asn Leu Ser Pro Asn Glu Thr Asn  
 405 410 415  
 Ala Thr Val Ser Asp Asn Val Ser Gln Ser Pro Thr Asn Pro Gly Glu  
 420 425 430  
 Ile Ser Gln Asn Glu Lys Gly Ile Cys Cys Asp Ser Gln Asn Asn Gly  
 435 440 445  
 Ser Glu Gly Val Ser Lys Pro Pro Ser Glu Ala Arg Leu Asn Ile Gly  
 450 455 460  
 His Leu Pro Ser Ala Lys Glu Ser Ala Ser Gln His Ile Thr Glu Glu  
 465 470 475 480  
 Glu Asp Asp Asp Pro Asp Val Tyr Tyr Phe Glu Ser Asp His Val Ala  
 485 490 495  
 Leu Lys His Asn Lys Asp Tyr Gln Arg Leu Leu Gln Thr Ile Ala Val  
 500 505 510  
 Leu Glu Ala Gln Arg Ser Gln Ala Val Gln Asp Leu Glu Ser Leu Gly  
 515 520 525  
 Arg His Gln Arg Glu Ala Leu Lys Asn Pro Ile Gly Phe Val Glu Lys  
 530 535 540  
 Leu Gln Lys Lys Ala Asp Ile Gly Leu Pro Tyr Pro Gln Arg Val Val  
 545 550 555 560  
 Gln Leu Pro Glu Ile Val Trp Asp Gln Tyr Thr His Ser Leu Gly Asn  
 565 570 575  
 Phe Glu Arg Glu Phe Lys Asn Arg Lys Arg His Thr Arg Arg Val Lys  
 580 585 590  
 Leu Val Phe Asp Lys Val Gly Leu Pro Ala Arg Pro Lys Ser Pro Leu  
 595 600 605  
 Asp Pro Lys Lys Asp Gly Glu Ser Leu Ser Tyr Ser Met Leu Pro Leu  
 610 615 620  
 Ser Asp Gly Pro Glu Gly Ser Ser Ser Arg Pro Gln Met Ile Arg Gly  
 625 630 635 640  
 Arg Leu Cys Asp Asp Thr Lys Pro Glu Thr Phe Asn Gln Leu Trp Thr  
 645 650 655  
 Val Glu Glu Gln Lys Lys Leu Glu Gln Leu Leu Ile Lys Tyr Pro Pro  
 660 665 670  
 Glu Glu Val Glu Ser Arg Arg Trp Gln Lys Ile Ala Asp Glu Leu Gly

|                                                                                    |     |     |
|------------------------------------------------------------------------------------|-----|-----|
| 675                                                                                | 680 | 685 |
| Asn Arg Thr Ala Lys Gln Val Ala Ser Arg Val Gln Lys Tyr Phe Ile<br>690 695 700     |     |     |
| Lys Leu Thr Lys Ala Gly Ile Pro Val Pro Gly Arg Thr Pro Asn Leu<br>705 710 715 720 |     |     |
| Tyr Ile Tyr Ser Lys Lys Ser Ser Thr Ser Arg Arg Gln His Pro Leu<br>725 730 735     |     |     |
| Asn Lys His Leu Phe Lys Pro Ser Thr Phe Met Thr Ser His Glu Pro<br>740 745 750     |     |     |
| Pro Val Tyr Met Asp Glu Asp Asp Asp Arg Ser Cys Phe His Ser His<br>755 760 765     |     |     |
| Met Asn Thr Ala Val Glu Asp Ala Ser Asp Asp Glu Ser Ile Pro Ile<br>770 775 780     |     |     |
| Met Tyr Arg Asn Leu Pro Glu Tyr Lys Glu Leu Leu Gln Phe Lys Lys<br>785 790 795 800 |     |     |
| Leu Lys Lys Gln Lys Leu Gln Gln Met Gln Ala Glu Ser Gly Phe Val<br>805 810 815     |     |     |
| Gln His Val Gly Phe Lys Cys Asp Asn Cys Gly Ile Glu Pro Ile Gln<br>820 825 830     |     |     |
| Gly Val Arg Trp His Cys Gln Asp Cys Pro Pro Glu Met Ser Leu Asp<br>835 840 845     |     |     |
| Phe Cys Asp Ser Cys Ser Asp Cys Leu His Glu Thr Asp Ile His Lys<br>850 855 860     |     |     |
| Glu Asp His Gln Leu Glu Pro Ile Tyr Arg Ser Glu Thr Phe Leu Asp<br>865 870 875 880 |     |     |
| Arg Asp Tyr Cys Val Ser Gln Gly Thr Ser Tyr Asn Tyr Leu Asp Pro<br>885 890 895     |     |     |
| Asn Tyr Phe Pro Ala Asn Arg<br>900                                                 |     |     |

## (2) INFORMATION FOR SEQ ID NO:143:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```

AATCGGGACC CCATCCCCCA AATCACTGGA TCCTGCAGCC CCACATCCTA AGGTGGATCC 60
CACGCTTCCC TGTGCCCCCT ACTGGATCCT GGACCTCTAC GTCTTAACCA CTGGATCCCA 120
CACAAATCAG TGAATGGATC CCAACACCCC AACCACAGGA GCACGGATTC CCTGTACCTC 180
AACACCCAGA CCCTGCCTCC CTCAGGCACC AGATCCAGTG TCCTAGTGAA ACGCTGGATC 240
CTAGATCCCC AACCCAGAT CCCCATGCCT CGAGCCCTGG ATCTCCAAGC TCAGCTGCTG 300

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GATTCTGGAT GTCAACAAAC CTCACCACTG GATCCTGACA ACCACAATGC CTGGATCCTG 360
GGGCCCCCAT CACTGGATCC CAGATCCCCT CACTCCACCC ACTGGATTCC TGCATTGGTT 420
TTTGGTTTTT TGTTTTTTTT TTAACCTCGA CACTGGGTCT CAGATCCTTC TGCTGACTGC 480
CAGATCCCTG CATTTCAAGC ACTACGCCTT CCACCCCCAG GCACTGGATC CCAGATTCCC 540
AAGCCTTCAC CCACCAGATT CTGGCTCCTA AAACAAGTGC GGGGGCCCCA GTGGCACAGC 600
AAGTGGATCC TGGCAACTGC AGCTGCTGGA TTCCAGATTG TGGGTCCCCA ATCCCTCTGC 660
CCAGTCCCTC AATGTTGAAA CCTCATCTCT TGAAGGCAGA TCCTGATATT CCAAGGCACT 720
GAATCCCAAG CCCTGAATCC CCGGTTTCTG ATCTGAATCT TCCAGGCGCC GGGTCCCAA 780
TGTTCAAGGC CCAAGTCTAG ATCCTGGCAG CCCAGTCACA GAGTATCCCCA CACACACTGG 840
TGCCCAGAGC CGGCTTCTCA TGACATGAAA TTGCATGGTC GAGGGAGTCT GTGGGGAAGG 900
AAGCCCAGGT CCTGGCTGCA ACCTGCACGG ATGCTGGATT CCCCTCACC CCACCTCTGC 960
ATGGCCACCC CCTCCCAGCC CTGTGGGGAA ACTGTTCCCT GGAACCACTC CACTCCCTGC 1020
ATCCCCACAC TTCACAGCAT CTTCATCCC CCTCCACTT CTAGGCGAAT AGTCCCCAGA 1080
GCTGTGTTCC TCCAAGGGGT CCGAGGAATC ACTACTCCT GGAGGCTGGC AAGGAGACAG 1140
TCTGAGGCCA GGGACACATG AAGGGATGTC CCCACCCAG CACTATCAGG GCCTCCCCAG 1200
GCTTCCAGAG TTGAAAGCCA GGAGAAAATC GGCAAAGACC ACCCTTCCCT AAACCCAAGC 1260
ACCCAATGAT GCRAAAAAAA AAAAAAAAAA AAAAAAAAAA 1299

```

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 98 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```

Met Lys Leu His Gly Arg Gly Ser Leu Trp Gly Arg Lys Pro Arg Ser
 1 5 10 15
Trp Leu Gln Pro Ala Arg Met Leu Asp Ser Pro Ser Pro His Leu Cys
 20 25 30
Met Ala Thr Pro Ser Gln Pro Cys Gly Glu Thr Val Pro Trp Asn His
 35 40 45
Ser Thr Pro Cys Ile Pro Thr Leu His Ser Ile Phe His Pro Pro Pro
 50 55 60
Thr Ser Arg Arg Ile Val Pro Arg Ala Val Phe Leu Gln Gly Val Arg
 65 70 75 80
Gly Ile Thr His Ser Trp Arg Leu Ala Arg Arg Gln Ser Glu Ala Arg
 85 90 95
Asp Thr

```

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 791 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```

CTCCTCTGTC CACTGCTTTC GTGAAGACAA GATGAAGTTC ACAATTGTCT TTGCTGGACT 60
TCTTGAGATC TTTCTAGCTC CTGCCCTAGC TAACTATAAT ATCAACGTCA ATGATGACAA 120
CAACAATGCT GGAAGTGGGC AGCAGTCAGT GAGTGTCAAC AATGAACACA ATGTGGCCAA 180
TGTTGACAAT AACACGGAT GGGACTCCTG GAATTCCATC TGGGATTATG GAAATGGCTT 240
TGCTGCAACC AGACTCTTTC AAAAGAAGAC ATGCATTGTG CACAAAATGA ACAAGGAAGT 300
CATGCCCTCC ATTCAATCCC TTGATGCACT GGTCAAGGAA AAGAAGCTTC AGGGTAAGGG 360
ACCAGGAGGA CCACCTCCCA AGGGCCTGAT GTACTCAGTC AACCCAAACA AAGTCGATGA 420
CCTGAGCAAG TTCGAAAAA ACATTGCAAA CATGTGTCGT GGGATTCCAA CATACTGGC 480
TGAGGAGATG CAAGAGGCAA GCCTGTTTTT TTACTCAGGA ACGTGCTACA CGACCAGTGT 540
ACTATGGATT GTGGACATTT CTTTCTGTGG AGACACGGTG GAGAACTAAA CAATTTTTTTA 600
AAGCCACTAT GGATTTAGTC ATCTGAATAT GCTGTGCAGA AAAAATATGG GCTCCAGTGG 660
TTTTTACCAT GTCATTCTGA AATTTTTTCTC TACTAGTTAT GTTTGATTTC TTTAAGTTTC 720
AATAAAATCA TTTAGCCTTG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 780
AAAAAAAAAA A

```

## (2) INFORMATION FOR SEQ ID NO:146:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

Met Lys Phe Thr Ile Val Phe Ala Gly Leu Leu Gly Val Phe Leu Ala
 1 5 10 15
Pro Ala Leu Ala Asn Tyr Asn Ile Asn Val Asn Asp Asp Asn Asn Asn
 20 25 30
Ala Gly Ser Gly Gln Gln Ser Val Ser Val Asn Asn Glu His Asn Val
 35 40 45
Ala Asn Val Asp Asn Asn Asn Gly Trp Asp Ser Trp Asn Ser Ile Trp
 50 55 60
Asp Tyr Gly Asn Gly Phe Ala Ala Thr Arg Leu Phe Gln Lys Lys Thr
 65 70 75 80
Cys Ile Val His Lys Met Asn Lys Glu Val Met Pro Ser Ile Gln Ser
 85 90 95
Leu Asp Ala Leu Val Lys Glu Lys Lys Leu Gln Gly Lys Gly Pro Gly
 100 105 110
Gly Pro Pro Pro Lys Gly Leu Met Tyr Ser Val Asn Pro Asn Lys Val
 115 120 125
Asp Asp Leu Ser Lys Phe Gly Lys Asn Ile Ala Asn Met Cys Arg Gly
 130 135 140
Ile Pro Thr Tyr Met Ala Glu Glu Met Gln Glu Ala Ser Leu Phe Phe
 145 150 155 160
Tyr Ser Gly Thr Cys Tyr Thr Thr Ser Val Leu Trp Ile Val Asp Ile
 165 170 175

```

Ser Phe Cys Gly Asp Thr Val Glu Asn  
180 185

## (2) INFORMATION FOR SEQ ID NO:147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2012 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```

CTCAAGTTCA TCATTGTCCT GAGAGAGAGG AGCAGCGCGG TTCTCGGCCG GGACAGCAGA 60
ACGCCAGGGG ACCCTCACCT GGGCGCGCGG GGGCACGGGC TTTGATTGTC CTGGGGTCGC 120
GGAGACCCGC GCGCCTGCCC TGCACGCCGG GCGGCAACCT TTGCAGTCGC GTTGGCTGCT 180
GCGATCGGCC GCGGGGTCCC TGCCGAAGGC TCGGCTGCTT CTGTCCACCT CTTACACTTC 240
TTCATTTATC GGTGGATCAT TTCGAGAGTC CGTCTTGTA ATGTTTGGA CTTTGCTACT 300
TTATTGCTTC TTTCTGGCGA CAGTTCACAG ACTCGCCGAG ACCGGCGGAG AAAGGCAGCT 360
GAGCCCGGAG AAGAGCGAAA TATGGGGACC CGGGCTAAAA GCAGACGTCG TCCTTCCCGC 420
CCGCTATTTT TATATTCAGG CAGTGGATAC ATCAGGGAAT AAATTCACAT CTTCTCCAGG 480
CGAAAAGGTC TTCCAGGTGA AAGTCTCAGC ACCAGAGGAG CAATTCAC TA GAGTTGGAGT 540
CCAGGTTTTT GACCGAAAAG ATGGGTCCTT CATAGTAAGA TACAGAATGT ATGCAAGCTA 600
CAAAAATCTG AAGGTGGAAA TTAAATTCCA AGGGCAACAT GTGGCCAAAT CCCCATATAT 660
TTTAAAAGGG CCGGTTTACC ATGAGAACTG TGA CTGTGCTT CTGCAAGATA GTGCAGCCTG 720
GCTACGGGAG ATGAACTGCC CTGAAACCAT TGCTCAGATT CAGAGAGATC TGGCACATTT 780
CCCTGCTGTG GATCCAGAAA AGATTGCAGT AGAAATCCCA AAAAGATTTG GACAGAGGCA 840
GAGCCTATGT CACTACACCT TAAAGGATAA CAAGGTTTAT ATCAAGACTC ATGGTGAACA 900
TGTAGGTTTT AGAATTTTCA TGGATGCCAT ACTACTTTCT TTGACTAGAA AGGTGAAGAT 960
GCCAGATGTG GAGCTCTTTG TTAATTTGGG AGACTGGCCT TTGGAAAAAA AGAAATCCAA 1020
TTCAAACATC CATCCGATCT TTTCTGGTG TGGCTCCACA GATTCCAAGG ATATCGTGAT 1080
GCCTACGTAC GATTTGACTG ATTCTGTTCT GGAAACCATG GGCCGGGTAA GTCTGGATAT 1140
GATGTCCGTG CAAGCTAACA CGGGTCCTCC CTGGGAAAGC AAAAATTCCA CTGCCGTCTG 1200
GAGAGGGCGA GACAGCCGCA AAGAGAGACT CGAGCTGGTT AAATCAGTA GAAAACACCC 1260
AGAACTCATA GACGCTGCTT TCACCAACTT TTTCTTCTTT AAACAGGATG AAAACCTGTA 1320
TGGTCCCATT GTGAAACATA TTTCAATTTT TGATTTCTTC AAGCATAAGT ATCAAATAAA 1380
TATCGATGGC ACTGTAGCAG CTTATCGCCT GCCATATTTG CTAGTTGGTG ACAGTGTTGT 1440
GCTGAAGCAG GATTCCATCT ACTATGAACA TTTTACAAT GAGCTGCAGC CCTGGAAACA 1500
CTACATTCCA GTTAAGAGCA ACCTGAGCGA TCTGCTAGAA AAATTAAT GGGCGAAAGA 1560
TCACGATGAA GAGGCCAAAA AGATAGCAAA AGCAGGACAA GAATTTGCAA GAAATAATCT 1620
CATGGGCGAT GACATATTCT GTTATTATTT CAACTYTTC CAGGAATATG CCAATTTACA 1680
AGTGAGTGAG CCCCAAATCC GAGAGGGCAT GAMAAGGGTA GAACCACAGA CTGAGGACGA 1740
CCTCTTCCST TGTACTTGCC ATAGGAAAAA GACCAAAGAT GAATSTGAT ATGCAAAATA 1800
ACTTCTATTA GAATAATGGT GCTCTGAAGA CTCTTCTTAA CTAAAAAGAA GAATTTTTTT 1860
AAGTATTAAT TCCATGGACA ATATAAAATC TGTGTGATTG TTTGCAGTAT GAAGACACAT 1920
TTCTACTTAT GCAGTATTCT CATGACTGTA CTTTAAAGTA CATTTT TAGA ATTTTATAAT 1980
AAAACCACCT TTATTTTAAA AAAAAAAAAA AA 2012

```

## (2) INFORMATION FOR SEQ ID NO:148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met Phe Gly Thr Leu Leu Leu Tyr Cys Phe Phe Leu Ala Thr Val Pro  
 1 5 10 15  
 Ala Leu Ala Glu Thr Gly Gly Glu Arg Gln Leu Ser Pro Glu Lys Ser  
 20 25 30  
 Glu Ile Trp Gly Pro Gly Leu Lys Ala Asp Val Val Leu Pro Ala Arg  
 35 40 45  
 Tyr Phe Tyr Ile Gln Ala Val Asp Thr Ser Gly Asn Lys Phe Thr Ser  
 50 55 60  
 Ser Pro Gly Glu Lys Val Phe Gln Val Lys Val Ser Ala Pro Glu Glu  
 65 70 75 80  
 Gln Phe Thr Arg Val Gly Val Gln Val Leu Asp Arg Lys Asp Gly Ser  
 85 90 95  
 Phe Ile Val Arg Tyr Arg Met Tyr Ala Ser Tyr Lys Asn Leu Lys Val  
 100 105 110  
 Glu Ile Lys Phe Gln Gly Gln His Val Ala Lys Ser Pro Tyr Ile Leu  
 115 120 125  
 Lys Gly Pro Val Tyr His Glu Asn Cys Asp Cys Pro Leu Gln Asp Ser  
 130 135 140  
 Ala Ala Trp Leu Arg Glu Met Asn Cys Pro Glu Thr Ile Ala Gln Ile  
 145 150 155 160  
 Gln Arg Asp Leu Ala His Phe Pro Ala Val Asp Pro Glu Lys Ile Ala  
 165 170 175  
 Val Glu Ile Pro Lys Arg Phe Gly Gln Arg Gln Ser Leu Cys His Tyr  
 180 185 190  
 Thr Leu Lys Asp Asn Lys Val Tyr Ile Lys Thr His Gly Glu His Val  
 195 200 205  
 Gly Phe Arg Ile Phe Met Asp Ala Ile Leu Leu Ser Leu Thr Arg Lys  
 210 215 220  
 Val Lys Met Pro Asp Val Glu Leu Phe Val Asn Leu Gly Asp Trp Pro  
 225 230 235 240  
 Leu Glu Lys Lys Lys Ser Asn Ser Asn Ile His Pro Ile Phe Ser Trp  
 245 250 255  
 Cys Gly Ser Thr Asp Ser Lys Asp Ile Val Met Pro Thr Tyr Asp Leu  
 260 265 270  
 Thr Asp Ser Val Leu Glu Thr Met Gly Arg Val Ser Leu Asp Met Met  
 275 280 285  
 Ser Val Gln Ala Asn Thr Gly Pro Pro Trp Glu Ser Lys Asn Ser Thr  
 290 295 300  
 Ala Val Trp Arg Gly Arg Asp Ser Arg Lys Glu Arg Leu Glu Leu Val  
 305 310 315 320

Lys Leu Ser Arg Lys His Pro Glu Leu Ile Asp Ala Ala Phe Thr Asn  
 325 330 335

Phe Phe Phe Phe Lys Gln Asp Glu Asn Leu Tyr Gly Pro Ile Val Lys  
 340 345 350

His Ile Ser Phe Phe Asp Phe Phe Lys His Lys Tyr Gln Ile Asn Ile  
 355 360 365

Asp Gly Thr Val Ala Ala Tyr Arg Leu Pro Tyr Leu Leu Val Gly Asp  
 370 375 380

Ser Val Val Leu Lys Gln Asp Ser Ile Tyr Tyr Glu His Phe Tyr Asn  
 385 390 395 400

Glu Leu Gln Pro Trp Lys His Tyr Ile Pro Val Lys Ser Asn Leu Ser  
 405 410 415

Asp Leu Leu Glu Lys Leu Lys Trp Ala Lys Asp His Asp Glu Glu Ala  
 420 425 430

Lys Lys Ile Ala Lys Ala Gly Gln Glu Phe Ala Arg Asn Asn Leu Met  
 435 440 445

Gly Asp Asp Ile Phe Cys Tyr Tyr Phe Lys Leu Phe Gln Glu Tyr Ala  
 450 455 460

Asn Leu Gln Val Ser Glu Pro Gln Ile Arg Glu Gly Met Xaa Arg Val  
 465 470 475 480

Glu Pro Gln Thr Glu Asp Asp Leu Phe Xaa Cys Thr Cys His Arg Lys  
 485 490 495

Lys Thr Lys Asp Glu Leu  
 500

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GNAAGAAGAG AGCAACAGCC AGGACCAAG

29

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

CNCAGGCTAG GCACTGATTC TGCTGGTTC

29

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GNAGACATGA AAGTTGAGCA GAAGGAAAG

29

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GNGGTGCTTT TGATATCCAG CCATCTCTA

29

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CNTGGAAAGA GGAGCAAGAA CCAAGGCAG

29

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TNGGTTTTGT ACGTTGTGCT CTTTTCATC

29

(2) INFORMATION FOR SEQ ID NO:155:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TNATGGTCTA TATAACTGTC CTCCTTCCT

29

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CNACACTGGG TCTCAGATCC TTCTGCTGA

29

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GNCTCCAAGA AGTCCAGCAA AGACAATTG

29

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ANTGCCAAAC ATTTACAAGA CGGACTCTC

29

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1776 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```

AGCTCACAGT AGCCCGGCGG CCCAGGGCAA TCCGACCACA TTTCACCTCTC ACCGCTGTAG 60
GAATCCAGAT GCAGGCCAAG TACAGCAGCA CGAGGGACAT GCTGGATGAT GATGGGGACA 120
CCACCATGAG CCTGCATTCT CAAGCCTCTG CCACAACCTCG GCATCCAGAG CCCC GGCGCA 180
CAGAGCACAG GGCTCCCTCT TCAACGTGGC GACCAGTGGC CCTGACCCTG CTGACTTTGT 240
GCTTGGTGCT GCTGATAGGG CTGGCAGCCC TGGGGCTTTT GTTTTTTTCAG TACTACCAGC 300
TCTCCAATAC TGGTCAAGAC ACCATTTCTC AAATGGAAGA AAGATTAGGA AATACGTCCC 360
AAGAGTTGCA ATCTCTTCAA GTCCAGAATA TAAAGCTTGC AGGAAGTCTG CAGCATGTGG 420
CTGAAAACCT CTGTCTGTGAG CTGTATAACA AAGCTGGAGC ACACAGGTGC AGCCCTTGTA 480
CAGAACAATG GAAATGGCAT GGAGACAATT GCTACCAGTT CTATAAAGAC AGCAAAAGTT 540
GGGAGGACTG TAAATATTTT TGCTTAGTG AAAACTCTAC CATGCTGAAG ATAAACAAAC 600
AAGAAGACCT GGAATTTGCC GCGTCTCAGA GCTACTCTGA GTTTTTCTAC TCTTATTGGA 660
CAGGGCTTTT GCGCCCTGAC AGTGGCAAGG CCTGGCTGTG GATGGATGGA ACCCCTTTCA 720
CTTCTGAAGT GTTCCATATT ATAATAGATG TCACCAGCCC AAGAAGCAGA GACTGTGTGG 780
CCATCCTTAA TGGGATGATC TTCTCAAAGG ACTGCAAAGA ATTGAAGCGT TGTGTCTGTG 840
AGAGAAGGGC AGGAATGGTG AAGCCAGAGA GCCTCCATGT CCCCCCTGAA ACATTAGGCG 900
AAGGTGACTG ATTCGCCCTC TGCAACTACA AATAGCAGAG TGAGCCAGGC GGTGCCAAAG 960
CAAGGGCTAG TTGAGACATT GGGAAATGGA ACATAATCAG GAAAGACTAT CTCTCTGACT 1020
AGTACAAAAT GGGTTCTCGT GTTTCCTGTT CAGGATCACC AGCATTCTCTG AGCTTGGGTT 1080
TATGCACGTA TTTAACAGTC ACAAGAAGTC TTATTTACAT GCCACCAACC AACCTCAGAA 1140
ACCCATAATG TCATCTGCCT TCTTGGCTTA GAGATAACTT TTAGCTCTCT TTCTTCTCAA 1200
TGTCTAATAT CACCTCCCTG TTTTCATGTC TTCCTTACAC TTGGTGGAAT AAGAAACTTT 1260
TTGAAGTAGA GGAAATACAT TGAGGTAACA TCCTTTTCTC TGACAGTCAA GTAGTCCATC 1320
AGAAATTGGC AGTCACTTCC CAGATTGTAC CAGCAAATAC ACAAGGAATT CTTTTTGTTC 1380
GTTTCAGTTC ATACTAGTCC CTTCCCAATC CATCAGTAAA GACCCCATCT GCCTTGTCCT 1440
TGCCGTTTCC CAACAGGGAT GTCACCTGAT ATGAGAATCT CAAATCTCAA TGCCCTTATA 1500
GCATTCCTTC CTGTGTCCAT TAAGACTCTG ATAATTGTCT CCCCTCCATA GGAATTTCTC 1560
CCAGGAAAGA AATATATCCC CATCTCCGTT TCATATCAGA ACTACCGTCC CCGATATTCC 1620
CTTCAGAGAG ATTAAAGACC AGAAAAAAGT GAGCCTCTTC ATCTGCACCT GTAATAGTTT 1680
CAGTTCCTAT TTTCTTCCAT TGACCCATAT TTATACCTTT CAGGTACTGA AGATTTAATA 1740
ATAATAAATG TAAATACTGT GAAAAAATAA AAAAAA 1776

```

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly
 1 5 10 15
Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His
 20 25 30
Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg
 35 40 45
Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly
 50 55 60

```

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn  
 65 70 75 80  
 Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr  
 85 90 95  
 Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly  
 100 105 110  
 Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys  
 115 120 125  
 Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His  
 130 135 140  
 Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp  
 145 150 155 160  
 Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn  
 165 170 175  
 Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe  
 180 185 190  
 Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala  
 195 200 205  
 Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile  
 210 215 220  
 Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu  
 225 230 235 240  
 Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val  
 245 250 255  
 Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro  
 260 265 270  
 Pro Glu Thr Leu Gly Glu Gly Asp  
 275 280

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

CAACTATCCC ATAATTTATT TATTCTTCTT CAATGTTTGT AAAGTGCATG AGTCATGTTC 60  
 ACACTTGAAG TCTAGTAGTG CACTGTAATA ATTCATTTTT TAAAAGATTA TTTAATGCCC 120  
 ATTTCAAAAT ACAGTAGTTT ACACAGCTAC AGAAACAATT TGGGGCAAGT TTTAAACAC 180  
 TGAAACAGTA ATAGTTATTG GTGTCACATA AACTGATTT GTTTTTTACA GCCAAACCTC 240  
 TGTCAGTCAG AGGCATTCAT TAGTTTATA CATGTAATTT GAAAATCACT AAACCTCGTT 300

```

TTCTCAGCAG CAATAATTTA AGAGGCTTCA AAAATATAAT TTCACTCTTA TTTAGTATTT 360
TTTCCTGGGG GGATTTTTTAC GTAATTTTTT TATGAAAAGA CAAATGCATG TTGAGATAAC 420
TTCTGGGATT AAAATAGTCT TTTGCTTTAC TTTTTTGGTT TCCTAAAACA ACTTTATTGA 480
CTTTTAGTCC ATACTGTTAT ATTTTGTCT TAAAGAAAAT TTAAACTACA AATACCAAAA 540
GAAAACATTT TAAATTTAGG GATGAGACTT TGGTGTATCG TGGGTCTAGG TTTAATGAAC 600
ACATCTGGGG TTAAGTTGGC ATTTCTTCAC ATCTCCACAC CCACACCAAC CATCACAGCC 660
CCCCACCAAC CTTCTCCCAA CCCCAAAAGC ATTGTCCAGG GATATAGATT TTACCAAAGG 720
CTTCCTGGGA AGACGAGGGA GCAACACTTT AGATTAAATG TGATCAGACT TTCCTATTAG 780
ATATGGCTCT TCTGTCTCTT GTTATCCCC TGACAGCTCT GCCATAAAGT CCCTTCTCCT 840
CATCCTTCCC AAACAGGCTG TATAAGTGCT TTGAGGTAAT TAAACTCTTT CCTCCAGTTT 900
ACAAATATCA CTTACAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAA 947

```

## (2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 72 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```

Met Arg Leu Trp Cys Ile Val Gly Leu Gly Leu Met Asn Thr Ser Gly
 1 5 10 15
Val Lys Leu Ala Phe Leu His Ile Ser Thr Pro Thr Pro Thr Ile Thr
 20 25 30
Ala Pro His Gln Pro Ser Pro Asn Pro Lys Ser Ile Val Gln Gly Tyr
 35 40 45
Arg Phe Tyr Gln Arg Leu Pro Gly Lys Thr Arg Glu Gln His Phe Arg
 50 55 60
Leu Asn Val Ile Arg Leu Ser Tyr
65 70

```

## (2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2120 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```

CGCTGACTTG GGCAATGGGG CCGGTGGGGT TTGGGGGCGG AAGAGACCCT CGGGGTTGAG 60
AAGTATGTGG TGGCCTTTCG TCCCCTGTAA AACATTGTCA CACGGTGTGG GGCGGCAGCG 120
CTGGATCTTT GCAAGGCTAT TTTGGCATTC TGCTGGATAT ATGTTCTGTA ATACCAAAGT 180
CGGCGGGAAA GTGAAGTTGT CTCCACCATA ACAGCAATTT TTTCTCTAGC AATTGCACTT 240
ATCACATCAG CACTTCTACC AGTGGATATA TTTTGGTTT CTTACATGAA AAATCAAAAT 300
GGTACATTTA AGGACTGGGC TAATGCTAAT GTCAGCAGAC AGATTGAGGA CACTGTATTA 360
TACGGTTACT ATACTTTATA TTCTGTTATA TTGTTCTGTG TGTTCTTCTG GATCCCTTTT 420
GTCTACTTCT ATTATGAAGA AAAGGATGAT GATGATACTA GTAAATGTAC TCAAATTAAA 480
ACGGCACTCA AGTATACTTT GGGATTTGTT GTGATTTGTG CACTGCTTCT TTTAGTTGGT 540

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GCCTTTGTTT CATTGAATGT TCCCAATAAC AAAAATTCTA CAGAGTGGGA AAAAGTGAAG 600
TCCCTATTTG AAGAACTTGG AAGTAGTCAT GGTTTAGCTG CATTGTCATT TTCTATCAGT 660
TCTCTGACCT TGATTGGAAT GTTGGCAGCT ATAACCTACA CAGCCTATGG CATGTCTGCG 720
TTACCTTTAA ATCTGATAAA AGGCACTAGA AGCGCTGCTT ATGAACGTTT GGAAAAACAT 780
GAAGACATTG AAGAAGTAGA ACAACACATT CAAACGATTA AATCAAAAAG CAAAGATGGT 840
CGACCTTTGC CAGCAAGGGA TAAACGCGCC TTAAAACAAT TTGAAGAAAAG GTTACGAACA 900
CTTAAGAAGA GAGAGAGGCA TTTAGAATTC ATTGAAAACA GCTGGTGGAC AAAATTTTGT 960
GGCGCTCTGC GTCCCCTGAA GATCGTCTGG GGAATATTTT TCATCTTAGT TGCATTGCTG 1020
TTTGTAATTT CTCTTTTCTT GTCAAATTTA GATAAAGCTC TTCATTGAGC TGGAATAGAT 1080
TCTGGTTTCA TAATTTTTTG AGCTAACCTG AGTAATCCAC TGAATATGCT TTTGCCTTTA 1140
CTACAAACAG TTTTCCCTCT TGATTATATT CTTATAACAA TTATTATTAT GTACTTTATT 1200
TTTACTTCAA TGGCAGGAAT TCGAAATATT GGCATATGGT TCTTTTGGAT TAGATTATAT 1260
AAAATCAGAA GAGGTAGAAC CAGGCCCCAA GCACTCCTTT TTCTCTGCAT GATACTTCTG 1320
CTTATTGTCC TTCACACTAG CTACATGATT TATAGTCTTG CTCCCAATA TGTATGTAT 1380
GGAAGCCAAA ATTACTTAAT AGAGACTAAT ATAACCTCTG ATAATCATAA AGGCAATTCA 1440
ACCCTTTCTG TGCCAAAGAG ATGTGATGCA GATGCTCCTG AAGATCAGTG TACTGTTACC 1500
CGGACATACC TATTCCTTCA CAAGTTCTGG TTCTTCAGTG CTGCTTACTA TTTTGGTAAC 1560
TGGGCTTTT TTTGGGTATT TTTGATTGGA TTAATTGTAT CCTGTTGTAA AGGGAAGAAA 1620
TCGGTTATTG AAGGAGTAGA TGAAGATTCA GACATAAGTG ATGATGAGCC CTCTGTCTAT 1680
TCTGCTTGAC AGCCTTCTGT CTTAAAGGTT TTATAATGCT GACTGAATAT CTGTTATGCA 1740
TTTTTAAAGT ATTAACTAA CATTAGGATT TGCTAACTAG CTTTCATCAA AAATGGGAGC 1800
ATGGCTATAA GACAACTATA TTTTATTATA TGTTTTCTGA AGTAACATTG TATCATAGAT 1860
TAACATTTTA AATTACCATA ATCATGCTAT GTAAATATAA GACTACTGGC TTTGTGAGGG 1920
AATGTTTGTG CAAAATTTTT TCCTCTAATG TATAATAGTG TTAAATTGAT TAAAAATCTT 1980
CCAGAATTAA TATTCCTTTT TGTCACTTTT TGAAAACATA ATAAATCATT TGTATCTGTG 2040
CCTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2100
AAAAAAAAAA AAAAAAAAAA

```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

```

Met Lys Asn Gln Asn Gly Thr Phe Lys Asp Trp Ala Asn Ala Asn Val
 1 5 10 15
Ser Arg Gln Ile Glu Asp Thr Val Leu Tyr Gly Tyr Tyr Thr Leu Tyr
 20 25 30
Ser Val Ile Leu Phe Cys Val Phe Phe Trp Ile Pro Phe Val Tyr Phe
 35 40 45
Tyr Tyr Glu Glu Lys Asp Asp Asp Thr Ser Lys Cys Thr Gln Ile
 50 55 60
Lys Thr Ala Leu Lys Tyr Thr Leu Gly Phe Val Val Ile Cys Ala Leu
 65 70 75 80
Leu Leu Leu Val Gly Ala Phe Val Pro Leu Asn Val Pro Asn Asn Lys
 85 90 95
Asn Ser Thr Glu Trp Glu Lys Val Lys Ser Leu Phe Glu Glu Leu Gly
 100 105 110

```

Ser Ser His Gly Leu Ala Ala Leu Ser Phe Ser Ile Ser Ser Leu Thr  
115 120 125

Leu Ile Gly Met Leu Ala Ala Ile Thr Tyr Thr Ala Tyr Gly Met Ser  
130 135 140

Ala Leu Pro Leu Asn Leu Ile Lys Gly Thr Arg Ser Ala Ala Tyr Glu  
145 150 155 160

Arg Leu Glu Asn Thr Glu Asp Ile Glu Glu Val Glu Gln His Ile Gln  
165 170 175

Thr Ile Lys Ser Lys Ser Lys Asp Gly Arg Pro Leu Pro Ala Arg Asp  
180 185 190

Lys Arg Ala Leu Lys Gln Phe Glu Glu Arg Leu Arg Thr Leu Lys Lys  
195 200 205

Arg Glu Arg His Leu Glu Phe Ile Glu Asn Ser Trp Trp Thr Lys Phe  
210 215 220

Cys Gly Ala Leu Arg Pro Leu Lys Ile Val Trp Gly Ile Phe Phe Ile  
225 230 235 240

Leu Val Ala Leu Leu Phe Val Ile Ser Leu Phe Leu Ser Asn Leu Asp  
245 250 255

Lys Ala Leu His Ser Ala Gly Ile Asp Ser Gly Phe Ile Ile Phe Gly  
260 265 270

Ala Asn Leu Ser Asn Pro Leu Asn Met Leu Leu Pro Leu Leu Gln Thr  
275 280 285

Val Phe Pro Leu Asp Tyr Ile Leu Ile Thr Ile Ile Ile Met Tyr Phe  
290 295 300

Ile Phe Thr Ser Met Ala Gly Ile Arg Asn Ile Gly Ile Trp Phe Phe  
305 310 315 320

Trp Ile Arg Leu Tyr Lys Ile Arg Arg Gly Arg Thr Arg Pro Gln Ala  
325 330 335

Leu Leu Phe Leu Cys Met Ile Leu Leu Leu Ile Val Leu His Thr Ser  
340 345 350

Tyr Met Ile Tyr Ser Leu Ala Pro Gln Tyr Val Met Tyr Gly Ser Gln  
355 360 365

Asn Tyr Leu Ile Glu Thr Asn Ile Thr Ser Asp Asn His Lys Gly Asn  
370 375 380

Ser Thr Leu Ser Val Pro Lys Arg Cys Asp Ala Asp Ala Pro Glu Asp  
385 390 395 400

Gln Cys Thr Val Thr Arg Thr Tyr Leu Phe Leu His Lys Phe Trp Phe  
405 410 415

Phe Ser Ala Ala Tyr Tyr Phe Gly Asn Trp Ala Phe Leu Gly Val Phe  
420 425 430

Leu Ile Gly Leu Ile Val Ser Cys Cys Lys Gly Lys Lys Ser Val Ile

435

440

445

Glu Gly Val Asp Glu Asp Ser Asp Ile Ser Asp Asp Glu Pro Ser Val  
 450 455 460

Tyr Ser Ala  
 465

## (2) INFORMATION FOR SEQ ID NO:165:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2487 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

```

GTTCCGAAAT AAAAGATTTT GCAAACCACT TTCCTACGTA CGTCCACTGT AGTTTTTGCA 60
GATACAACAC TAGCTGTAGC AAAGCCTATG TAAATCATAT GATGAGCTTT CATAGTAACC 120
GTCCAAGCAA AAGGTTTTGT ATTTTAAAGA AGCATTCAGA AAATCTCCGG GGCATTACTC 180
TAGTGTGCCT TAATTGTGAT TTCCTAAGTG ATGTTTCTGG CTTAGATAAT ATGGCTACAC 240
ACTTAAGTCA ACATAAACT CATACTTGCC AAGTTGTAAT GCAGAAAGTT TCTGTTTGTA 300
TCCCAACTTC TGAGCACCTT TCTGAATTAA AAAAAGAAGC TCCCGCAAAG GAACAAGAAC 360
CTGTGTCTAA GGAAATTGCA AGACCTAACA TGGCTGAAAG AGAAACAGAA ACATCAAATT 420
CTGAAAGTAA ACAAGATAAA GCTGCTTCTT CAAAAGAAAA AAATGGATGT AATGCAAATT 480
CATTTGAAGG CTCATCAACA ACAAAAAGTG AAGAAAGCAT AACAGTTTCA GATAAGGAAA 540
ATGAAACCTG TCTTGACAGC CAGGAACTG GCTCAAAAAA CATCGTCAGT TGTGATTCAA 600
ATATTGGTGC AGATAAAGTG GAAAAGAAAA AACAAATACA ACACGTTTGT CAGGAAATGG 660
AGTTGAAGAT GTGCCAAAGT TCAGAAAACA TAATCTTATC TGATCAGATT AAAAGTCACA 720
ACTCCAGTGA AGCCAGATTT TCTTCAAAGA ATATTAAGGA TTTGCGATTA GCATCAGATA 780
ATGTAAGCAT TGATCAGTTT TTGAGAAAAA GACATGAACC TGAATCTGTT AGTTCTGATG 840
TTAGCGAGCA AGGCAGTATT CATTTGGAAC CTCTGACTCC ATCCGAGGTA CTTGAGTATG 900
AAGCCACAGA GATTCTTCAG AAAGGTAGTG GTGATCCTTC AGCCAAGACT GATGAAGTAG 960
TGTCTGATCA AACAGATGAC ATTCTTGGAG GAAATAACCC TAGCACAACA GAGGCAACAG 1020
TAGACCTGGA AGATGAAAAA GAAAGAAGTT GAAATTAGTC ATTTTAAGTT TCAGTGTACC 1080
AACGATAAGG GCATTGGGAA CAGTGCTATC AGGTGAGCTC AGTGGTGCTG TTGTAGGTTT 1140
AGAAATGGAA ATATGTAAGG GAGGTCACAC ATACACTTTA CCTGTATGTT CAACCTATG 1200
TATCAAACAA ATCAATTCAC CAATAATAGC ATGATTAGTA GGGATTCCCA AAAAGTTTTT 1260
AAAAACACGA ACAGGATTTT AATGATAATT AAATTGTCAG TGGAAAGGTC TCATTTAATG 1320
GTTTTCAAGG AAATGGGATT TGGTTGCTGA CATGAATTGA TGATATTAGT AATATTTATA 1380
AAGCCTTTCA AACTTCCATC AATCCTAAGC TAAAAATCTT TATTACCTGT ATATCCTTTT 1440
CAGTTAACTG AGAGGAAGGG ATTTGGAAAC CATGTACTTT TGGGGAGTAA TTGATTAAAA 1500
ACAATGGCTG ATTGGCATTG TTAATGAAGG CTTTATTTGT GAGGATGATG CTGGTAAATG 1560
GAGCATGCTT AGAGTACTAA ATTGATCTAA TGAGAATTTG GATGAACATA AACTTAATTT 1620
TGGATTTAAT ATAACATTCC AGTCAGACGC ATGTAAACAG AATATTTGAA TCTTTGTACC 1680
TCCATACAAG TGTTAGCCTG CCAGGCTGTA AGCTTACCTT AATTAACTT TCAGTGAAAG 1740
TGGAATTATT AAGATATAAA TTTATATTTG TGCTTTTTGT CAGTGTGTAA GCTGTGTAGA 1800
AATTCCTTTG TGTATTAGTT GTATTAATGT AAAGTAGAAA CCCATTGTTG AAACCTCTGT 1860
AGCTATTATG CTTTAAATAT TGTTTAATG ATCTTCCTTA GAAATAGGCC CATAAAAATG 1920
GTCTGGAAGC CAAACCAAAG TATGGTATAA TGATAGATATT GTAAAGCAGT AAACGTAAAA 1980
CATGTCCTGG CATGTATTCA GCCATGTTTA AGTGACTTTT CTGTAATTGT AAAATAAAAA 2040
CTTCAAATGG GACCTAAAC AGTGATGTAA AAGAACTGGT TTTGGAAATT TAGCCTAATT 2100
TATCTATAAG ATGGCTGCTA AATTGATTTT TCAGTTCTTT TTATCATCTA GAATATAATA 2160
GATAGATAAA TGAATAATAT GAAGAACAGT AGTTTGCTTT GAAATACTAA TAACTTTTAA 2220
TTTAAATGCT TTCATTTTAA CTTCTTAAAA TGTGCTTTGG ATTCTTAAAT TTTGTTTAC 2280
TGAATGTTCA ATGTTTTTAA TGGCGATTAA AATACTCTGC TGTATATAGT AGTTTTTGAG 2340

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TAAATATTTG CAATAAAAAT CTGCCCCCGA ATAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2400  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2460  
 AAAAAAAAAA AAAAAAAAAA AAAAAA 2487

## (2) INFORMATION FOR SEQ ID NO:166:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met Met Ser Phe His Ser Asn Arg Pro Ser Lys Arg Phe Cys Ile Phe  
 1 5 10 15

Lys Lys His Ser Glu Asn Leu Arg Gly Ile Thr Leu Val Cys Leu Asn  
 20 25 30

Cys Asp Phe Leu Ser Asp Val Ser Gly Leu Asp Asn Met Ala Thr His  
 35 40 45

Leu Ser Gln His Lys Thr His Thr Cys Gln Val Val Met Gln Lys Val  
 50 55 60

Ser Val Cys Ile Pro Thr Ser Glu His Leu Ser Glu Leu Lys Lys Glu  
 65 70 75 80

Ala Pro Ala Lys Glu Gln Glu Pro Val Ser Lys Glu Ile Ala Arg Pro  
 85 90 95

Asn Met Ala Glu Arg Glu Thr Glu Thr Ser Asn Ser Glu Ser Lys Gln  
 100 105 110

Asp Lys Ala Ala Ser Ser Lys Glu Lys Asn Gly Cys Asn Ala Asn Ser  
 115 120 125

Phe Glu Gly Ser Ser Thr Thr Lys Ser Glu Glu Ser Ile Thr Val Ser  
 130 135 140

Asp Lys Glu Asn Glu Thr Cys Leu Ala Asp Gln Glu Thr Gly Ser Lys  
 145 150 155 160

Asn Ile Val Ser Cys Asp Ser Asn Ile Gly Ala Asp Lys Val Glu Lys  
 165 170 175

Lys Lys Gln Ile Gln His Val Cys Gln Glu Met Glu Leu Lys Met Cys  
 180 185 190

Gln Ser Ser Glu Asn Ile Ile Leu Ser Asp Gln Ile Lys Asp His Asn  
 195 200 205

Ser Ser Glu Ala Arg Phe Ser Ser Lys Asn Ile Lys Asp Leu Arg Leu  
 210 215 220

Ala Ser Asp Asn Val Ser Ile Asp Gln Phe Leu Arg Lys Arg His Glu  
 225 230 235 240



Pro Glu Ser Val Ser Ser Asp Val Ser Glu Gln Gly Ser Ile His Leu  
 245 250 255

Glu Pro Leu Thr Pro Ser Glu Val Leu Glu Tyr Glu Ala Thr Glu Ile  
 260 265 270

Leu Gln Lys Gly Ser Gly Asp Pro Ser Ala Lys Thr Asp Glu Val Val  
 275 280 285

Ser Asp Gln Thr Asp Asp Ile Pro Gly Gly Asn Asn Pro Ser Thr Thr  
 290 295 300

Glu Ala Thr Val Asp Leu Glu Asp Glu Lys Glu Arg Ser  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

TTTATTTTTC AAATCATAAT TTTAAAATGA TAGATACCAT TTTGTGATAA CAACAATTCA 60  
 GAAAACAATT TTCTATCCTC TTAGTTGAAA GAATGTAGGT ACAGTTTGGA TACTTGACT 120  
 TTAATTTTAG AGTAAACATC TGCATTATAC TCTTATAGAT AATAGAATTA TTTAGTTAAG 180  
 AAATTCCTTA CAGTAAATGA GATAATGTGT GAAAAAGTAT TTTGTAAATG CTGAGGATTC 240  
 TACAAATGAT AGTTGTTATT TTCATGTGTA TTTGTAAGAT CATGTCCATT TCATGAATAT 300  
 AGGACTTCAC ATAAAAAAG ACTTCTCTCA GACAACCTTA TATTCTAGTA TTTTCTGTT 360  
 GTAAAAAGTA TTAATATTT ACTTTTATTT TGTTATACAT TTATTTTAAT ATCCATGTGT 420  
 TTATTATAGT AAATTTGAAA TGAAATCCTG AAAAACAGAA TTTTTTTTAA CACAGACCTC 480  
 ACACCAATAT TAATTTTTTC TCTACATAAT TTAATACTAC ATAAATTAAG TACTTAAAAT 540  
 TTATATTGAA GGCCACCAAG AACTTAGGTT GAATCTTAGA AAATTTAAAT AACTATTTTT 600  
 AAAGTTACCC AACTTAATAT TTTAATTTTT TAATATTTAT CTTCCCTTAC TAATTCTTGA 660  
 TAAATAATAG CATTAGACTT GATAAAATAA AAAAGAATTT TAGAGTAGAA TTAATATATC 720  
 AAAAGGGGTA TATCAACCAA ATTGGTGTCA GATTGTATTC ATTCTCTCAT CACATAAAGA 780  
 TTTTCTTTTT GATAGGTGAT GCTCATATGA ACCTTTGGTT TAGAATCTAT ATATGTACAT 840  
 GTGTATGTAT GTAGATAGTA TGGTTGTATA CACACATATA TACCAAACAC CATGAATTTT 900  
 AGCAGTCTGT GATGATCAGC AAAAAAGCAC ATAAAGTAAA ATTAGTTGAC CATGCTAAAT 960  
 TCAATTCTGG AATTTTTTTT TATTTGGGCA TTTCTAGAAC TTTTACATT TGAAAGTACA 1020  
 TGATGAGTAT TAGTAACGAT GACTTATGTA TAATCAGAAT CTTTATGACA ATTTAGTTTT 1080  
 ACAAGGTCAG AAGAGATGAG TTTGCTAAAC CCAGCTGTGA TACCTCAGTT GGAAAGGGAA 1140  
 TTCAAAGGTA TGCTTTGTAG AACAGAAAAG TATAGTTTTT TTTTCATGAA CTTAATCAT 1200  
 TTTCTGTTTT TCCTCTATGT GAGTCAGCTA CAAAAGTGGT CTAATTTTTA CAACAGTAGA 1260  
 ACTTCCTCCT TTTCTACTGT AATCTTCCCA CTGACTTTAC TGCACAGGTA TGAAATACTA 1320  
 GTGTATTGGA TCTTCAGTAA CCTTTTTATT TCCTAGATGA TTGAAATATA GGTATTTACT 1380  
 CCATTTAAAC CAGGTGATAA GATGATGTAA ATACTCAGGG AGGGTATTAA CTGTGTACTT 1440  
 TTGCTCGTTT GGGGTGTAAA GTGCCATGAC TGAATAATCT TCAATTCTATG ATTCTAGAGT 1500  
 AAGTTTAATT TGGAAAAGG GGCTTCACAC ATGGTGGTGG TTGAACATTG ATTCTTTTAT 1560  
 ACTTAAAAAG ATGAAAATGT TTTGTGGACT GATACATTTT ATCTTACTGA ATATGAATTG 1620  
 TTTATGTATC TCTACTGTCA AATAGCCTTT TTGAACTCA GGAAAGACAA AGGTTCAATT 1680  
 ACACCACTTT TGTCATAAAG CAAACCAGGT ATTTTTTTTT TCTCCTGTTG TCTGGATATG 1740  
 GCAATAGATT TTTTAAATTG CTGTGAGAAC CCATATATGA AAAGAGAGGA GTTGAATTGT 1800  
 GTGTGCCTTT TATGTCTTGA GATTTATATG TGGAAAAGAC GACATCTACT TCAAACGTGA 1860  
 TTTTTTCGTT TTTTTTTTTT TTTTGGGGA AGGGGGGAGA ACGGGGTCTT GCTCTGTCCG 1920

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CCAGGCTGGA GTGCAGTGGC GCGATCTCAG CTGACTGCAA CCTCCACCTC CCGGGTTCAA 1980
GGGATTCTGC CTCAGCCTCC CGAGTAGCTG AGACCACAGG TGCCTGCCAC CACACCCGGC 2040
TAATTTTTTT GTATTTTTAG TAGAGACGGG GTTTAGTAGA GACGGATCAC TCCTGACCAC 2100
GTGATCCGCC CACCTCGGCC TCCCAAAGTG CTGGGATTAC AGGCGTGAGC CACCACCCCC 2160
GGCCTGTATT TTCAGAGAGG AGAGCTTGGT GTTTTTGTGG TGCCAAGTGG TAAGATAATG 2220
TCTCTTTGAG GCTTCCTATG GACTGCCTTT ATTTTAGTAA ACTCAAGACA CCAGTTAACC 2280
TCAACAGAGT TTTGGCCTTA TTAGAATTTG TTGTGCATCT TATTGAAAGC CAGGTTTACA 2340
TCACCTCACC CCATTATTCT TTTTAGTTAA ATAAATTTAC CATGCCAAGT AACCAGAATG 2400
GAGCAAATTG GTTGATCTTT AAGGCAGTAG GTTTGACTAG CTAGCTATCA TTATTGTCAC 2460
ATCTAATGCT AGGCACCAGA AACCATTTGA GCCAGGAGTG TGAATGAATA ATTCCCAGAG 2520
ACACTTTAGA CATTTTTTAA TGTTTTATAT GACATTTTAC ATTTGTGTGA TTGCCTTAGA 2580
TATTAAATTT TCCTAGTGCT GATAAAAACA GCAACATTCA TAACTTATTT TATATATTGT 2640
TCCAAAGAAA AGAATTTGTT TTAATGGTTT CAAAATAACT GCACCTGAAT TTGTTTATGT 2700
GCCTTAAGTT CTCTAGTGCT ATTTCAACTT TTTTTTCAAT CTAAATGAAG CTTACCTTAG 2760
ATAAGGTTCA TATTTGTTTC CTATAGAGTA AATAAACTTC CCCTTCTTAA ATTGTGTAAT 2820
AAGCACCAAC GTGTGGTTGC TTGGCAGAAT GAGAATGTTA AGGGAGATTG TTGGATGTTT 2880
GGAGTTTCAT TATATTTTTT GTTTTTATTT TTTGATACCT AGGTGCTTTT TAAATATTTT 2940
AGACAAATAT CTATCTTACA TTGATTAAAC CCGTGTAAT TCATTTGCAG TATCTACATC 3000
GAATGTCAAA AAAGTATACT TATTTTTGTT CCATACTTAT GTACAATTTT TTCCCTCTTC 3060
AGGCTTTTTT ATTTACCTTT TTGAAAAGC ACTTACTCTC CCCTTCCCTA TCACCCCTCC 3120
CCCAAGGTTT CTTTATTTAA ATTTTATTG AGAGTTGTTG GAGCTCTAAG ACAATACAAA 3180
TTTAGAGTTG AACAAAAGTA TAATCTGCTT TACAAC TAGT TACATGTTT GTTTAAATAT ACTTCTTGCA 3360
TAGTTAAGTT GTAGCACGTG AATACTTACT TACATGTTT GTTTAAATAT ACTTCTTGCA 3360
TAGTTAAGTT GTAGCACGTG AATACTTACT TACATGTTT GTTTAAATAT ACTTCTTGCA 3360
TAGTTAAGTT GTAGCACGTG AATACTTACT TACATGTTT GTTTAAATAT ACTTCTTGCA 3360
ATATGGTTGT ATTAAATTTT GTTTACGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3480
AAAAAAAAAA AAAAA 3495

```

## (2) INFORMATION FOR SEQ ID NO:168:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

```

Met Ser Lys Lys Tyr Thr Tyr Phe Cys Ser Ile Leu Met Tyr Asn Phe
 1 5 10 15
Phe Pro Leu Gln Ala Phe Ser Phe Thr Phe Leu Lys Lys His Leu Leu
 20 25 30
Ser Pro Ser Leu Ser Pro Leu Pro Gln Gly Phe Phe Ile
 35 40 45

```

## (2) INFORMATION FOR SEQ ID NO:169:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

```

GTTGATCCAT CTGAGAAAGG GATCATGAAC TAGACAGAAT GAACAGCCTT AGAGGCACAG 60
ACTCTTGAAC GGGACGGTGG TGGTATGACT AGTGCAGAGT GTTTAGAGAT CACTCAGTTT 120
TTAAAGACTG GCCTTTATCG TGTCTCAGTG CAGCCGAGGC AGAGCCTTTG AAGGATGCGA 180
TGTTGTCATT CTTACTAATC TAGTCCAGCC GCTGAGGTGA CTTTCAACGG CAGACCGTCT 240
CCTGAGCGCC CCAGGTAGAA TTTCAAAGT CTCCGGGACC ATTATGGCAG TCAAGTGGAC 300
GGGTGGGCAT TCTTCTCCTG TCCTCTGCCT GAATGCAAGT AAAGAAGGGC TGCTGGCTTC 360
TGGAGCAGAG GGGCGGAGATC TCACGGCTTG GGGTGAAGAT GGAAGTCCAT TAGGACACAC 420
GCGGTTCCAA GGGGCTGATG ATGTTACCAG TGTCTTATTT TCTCCCTCCT GTCCCACCAA 480
GCTCTATGCC TCACATGGAG AAACCATTAG TGTACTGGAT GTCAGGTCCC TCAAAGATTC 540
CTTGACCAT TTTTCATGTA ATGAAGAAGA AATCAATTGT CTTTCATTGA ATCAAACGGA 600
AAACCTGCTG GCTTCTGCTG ACGACTCTGG GGCAATCAAA ATCCTAGACT TGGAAAACAA 660
GAAAGTTATC AGATCCTTGA AGAGACATTC CAATATCTGC TCCTCAGTGG CTTTTCGGCC 720
TCAGAGGCCT CAGAGCCTGG TGTCATGTGG ACTGGATATG CAGGTGATGC TGTGGAGTCT 780
TCAAAAAGCC CGACCACTCT GGATTACAAA TTTACAGGAG GATGAAACAG AAGAAATGGA 840
AGGCCACAG TCACCTGGTC AGCTCTTAAA CCCTGCCCTA GCCCATTCTA TCTCTGTGGC 900
TTCGTGTGGT AATATTTTTT GTTGTGGTGC AGAAGATGGT AAGGTTTCGAA TCTTTCGGGT 960
GATGGGAGTT AAGTGTGAAC AGGAACTGGG ATTTAAGGGC CACACTTCAG GGGTATCCCA 1020
GGTCTGCTTT CTCCCAGAAT CCTATTTGCT GCTTACTGGA GGAATGATG GGAAGATCAC 1080
GTTGTGGGAT GCAAACAGTG AAGTTGAGAA AAAACAGAAG AGTCCCACAA AACGTACCCA 1140
CAGGAAGAAA CCTAAAAGAG GAACTTGCAC CAAGCAGGGT GGAAATACTA ACGCTTCAGT 1200
AACAGATGAG GAAGAACATG GCAACATTTT ACCGAAGCTA AATATTGAAC ATGGAGAAAA 1260
AGTGAAGTGG CTCTTGGGTA CAAAATAAAA GGGACACCAA AATATATTAG TAGCTGATCA 1320
AACTAGTTGT ATATCTGTAT ACCCCTTAAA TGAATTTTAA ATCCAATAAA AACATTTGAA 1380
GAAAAAAAAA AAAAAAAA

```

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```

Met Ala Val Lys Trp Thr Gly Gly His Ser Ser Pro Val Leu Cys Leu
 1 5 10 15
Asn Ala Ser Lys Glu Gly Leu Leu Ala Ser Gly Ala Glu Gly Gly Asp
 20 25 30
Leu Thr Ala Trp Gly Glu Asp Gly Thr Pro Leu Gly His Thr Arg Phe
 35 40 45
Gln Gly Ala Asp Asp Val Thr Ser Val Leu Phe Ser Pro Ser Cys Pro
 50 55 60
Thr Lys Leu Tyr Ala Ser His Gly Glu Thr Ile Ser Val Leu Asp Val
 65 70 75 80
Arg Ser Leu Lys Asp Ser Leu Asp His Phe His Val Asn Glu Glu Glu
 85 90 95
Ile Asn Cys Leu Ser Leu Asn Gln Thr Glu Asn Leu Leu Ala Ser Ala
100 105 110

```

Asp Asp Ser Gly Ala Ile Lys Ile Leu Asp Leu Glu Asn Lys Lys Val  
115 120 125

Ile Arg Ser Leu Lys Arg His Ser Asn Ile Cys Ser Ser Val Ala Phe  
130 135 140

Arg Pro Gln Arg Pro Gln Ser Leu Val Ser Cys Gly Leu Asp Met Gln  
145 150 155 160

Val Met Leu Trp Ser Leu Gln Lys Ala Arg Pro Leu Trp Ile Thr Asn  
165 170 175

Leu Gln Glu Asp Glu Thr Glu Glu Met Glu Gly Pro Gln Ser Pro Gly  
180 185 190

Gln Leu Leu Asn Pro Ala Leu Ala His Ser Ile Ser Val Ala Ser Cys  
195 200 205

Gly Asn Ile Phe Ser Cys Gly Ala Glu Asp Gly Lys Val Arg Ile Phe  
210 215 220

Arg Val Met Gly Val Lys Cys Glu Gln Glu Leu Gly Phe Lys Gly His  
225 230 235 240

Thr Ser Gly Val Ser Gln Val Cys Phe Leu Pro Glu Ser Tyr Leu Leu  
245 250 255

Leu Thr Gly Gly Asn Asp Gly Lys Ile Thr Leu Trp Asp Ala Asn Ser  
260 265 270

Glu Val Glu Lys Lys Gln Lys Ser Pro Thr Lys Arg Thr His Arg Lys  
275 280 285

Lys Pro Lys Arg Gly Thr Cys Thr Lys Gln Gly Gly Asn Thr Asn Ala  
290 295 300

Ser Val Thr Asp Glu Glu Glu His Gly Asn Ile Leu Pro Lys Leu Asn  
305 310 315 320

Ile Glu His Gly Glu Lys Val Asn Trp Leu Leu Gly Thr Lys Ile Lys  
325 330 335

Gly His Gln Asn Ile Leu Val Ala Asp Gln Thr Ser Cys Ile Ser Val  
340 345 350

Tyr Pro Leu Asn Glu Phe  
355

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

```

CCGGAGGTAG CTACCACGGC CTGTGTCAAC GACTAAAGCT CCAGTACAGC GGCGCCCTCA 60
GACAGCTGGG AGGGTGGCTC TGGCCGGGAG CGGCGGCCGG TGAGCTACCG CGAGGAGGAG 120
CGGCGGAGGC GACCTCGGCC CGGCCCTGCA CTGGCCGCCC GGCAGGCGCG ACATGAGCCT 180
GGTCTGGCAT CCGCGGGATG CTCCTTAAGC CCCTTCTCCG GCTGTTAACC TCCGGGGAAC 240
GGTTGTGACC ACACCGACAC GTATTTTACA GATAAATCAT TCTTGCGGCG GCGGGTCGAA 300
CACGTTTATT TATTTTTTAT TTTCTCAACA AGCTTTTACC CAGCACCTGT CCAGTGAAAC 360
AACTTGATAA TCGTTTCGAG GGGCGTCCGC CGGGTTAGGA AGCCACTGCC TGGCAGCTTG 420
TGGAAGCCTC ATTTGCAAAG CCACCCCTCA GATGTTTGA AGATCGTGAC GTCTTGTAAC 480
TAGCAGTGTG TGCACAGAAT CCTACTCAAG GAACGTCTTG GCCCAGCGAT GCAAAGAACT 540
GAAGTTTCAA GCTGGAAGAG CCTGTATTGT CCTCACAATA GTATAGAAGA ATTCAGAGA 600
GGAGAGAGAG ACAGCACCGA ATGAAGACTG TAAAAGAAAA GAAGGAATGC CAGAGATTGA 660
GAAAATCTGC CAAGACTAGG AGGGTAACCC AGAGGAAACC GTCTTCAGGG CCTGTTTGCT 720
GGCTATGCCT TCGAGAACCT GGGGATCCCG AAAAATTAGG GGAATTTCTT CAGAAAGACA 780
ATATCAGCGT GCATTATTTC TGTCTTATCT TATCTAGTAA GCTGCCTCAG AGGGGCCAGT 840
CCAACAGAGG TTTCCATGGA TTTCTGCCTG AAGACATCAA AAAGGAGGCA GCCCGGGCTT 900
CTAGGAAGAT CTGCTTTGTG TGCAAGAAAA AGGGAGCTGC TATCAACTGC CAGAAGGATC 960
AGTGCCTCAG AAACCTCCAT CTGCCTTGTC GCCAAGAAAG GGGTTGCCTT TCACAATTTT 1020
TTGGAGAGTA CAAATCATTT TGTGACAAAC ATCGCCCAAC ACAGAACATC CAACATGGGC 1080
ATGTGGGGGA GGAAAGCTGC ATCTTATGTT GTGAAGACTT ATCCAACAG AGTGTTGAGA 1140
ACATCCAGAG CCCGTGTTGT AGTCAAGCCA TCTACCACCG CAAGTGCATA CAGAAATATG 1200
CCCACACATC AGCAAAGCAT TTCTTCAAT GTCCACAGTG TAACAATCGA AAAGAGTTTC 1260
CTCAAGAAAT GCTGAGAATG GGAATTCATA TTCCAGACAG AGATGCTGCC TGGGAACTCG 1320
AGCCAGGGGC TTTCTCAGAC TTATATCAGC GTATACAGCA CTGTGATGCC CCCATCTGTC 1380
CGTATGAACA AGGCAGAGAC AGCTTTGAGG ATGAAGGGAG GTGGTGCCTC ATTCTGTGTG 1440
CTACATGCGG ATCCCACGGA ACCCAGAGGG ACTGCTCCTC TCTTAGATTT AACAGTAAGA 1500
AATGGGAGTG TGAGGAGTGT TCACCTGCTG CAGCCACAGA CTACATACCT GAAAACCTCAG 1560
GGGACATCCC TTGCTGCAGC AGCACCTTCC ACCCTGAGGA ACATTTCTGC AGAGACAACA 1620
CCTTGGAAGA GAATCCGGGC CTTTCTTGGA CTGATTGGCC AGAACCTTCC TTATTAGAAA 1680
AGCCAGAGTC CTCTCGTGGC AGGAGGAGCT ACTCCTGGAG GTCCAAGGGT GTCAGAATCA 1740
CTAACAGCTG CAAAAAATCC AAGTAACACC TTCTGAGTAG CTGCTGTCCC ACACAATAGG 1800
GTATGAAGCT GCGCTCCTCC ATCGGGTTTG GGGAGGGAGC ACTCTGGGAC TGTGAGACAA 1860
GGAAGCAGGG CCAGCAGTGA GACTATGAGC CAAGCAAAGA GAAGTCTCAG TGGAGCATGA 1920
GGAGGGAGCA GTCCAGATGC CAACAAGGAA ATGCGTTTAT GGCTACAAGA GTGCCCTCTGC 1980
TTTCTCCTCC TCTCCTCCCA CCAAGGATTC TTCCACCTTA ATCTTGTTTT CATATGCCCTC 2040
TTCTTACTTC ACCCATGTTT GTTGTTATGC AAATAAAGGT TTTCTCTCCC AAAAAAAAAA 2100
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA 2132

```

## (2) INFORMATION FOR SEQ ID NO:172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```

Met Lys Thr Val Lys Glu Lys Lys Glu Cys Gln Arg Leu Arg Lys Ser
 1 5 10 15
Ala Lys Thr Arg Arg Val Thr Gln Arg Lys Pro Ser Ser Gly Pro Val
 20 25 30
Cys Trp Leu Cys Leu Arg Glu Pro Gly Asp Pro Glu Lys Leu Gly Glu
 35 40 45
Phe Leu Gln Lys Asp Asn Ile Ser Val His Tyr Phe Cys Leu Ile Leu
 50 55 60

```

Ser Ser Lys Leu Pro Gln Arg Gly Gln Ser Asn Arg Gly Phe His Gly  
 65 70 75 80  
 Phe Leu Pro Glu Asp Ile Lys Lys Glu Ala Ala Arg Ala Ser Arg Lys  
 85 90 95  
 Ile Cys Phe Val Cys Lys Lys Lys Gly Ala Ala Ile Asn Cys Gln Lys  
 100 105 110  
 Asp Gln Cys Leu Arg Asn Phe His Leu Pro Cys Gly Gln Glu Arg Gly  
 115 120 125  
 Cys Leu Ser Gln Phe Phe Gly Glu Tyr Lys Ser Phe Cys Asp Lys His  
 130 135 140  
 Arg Pro Thr Gln Asn Ile Gln His Gly His Val Gly Glu Glu Ser Cys  
 145 150 155 160  
 Ile Leu Cys Cys Glu Asp Leu Ser Gln Gln Ser Val Glu Asn Ile Gln  
 165 170 175  
 Ser Pro Cys Cys Ser Gln Ala Ile Tyr His Arg Lys Cys Ile Gln Lys  
 180 185 190  
 Tyr Ala His Thr Ser Ala Lys His Phe Phe Lys Cys Pro Gln Cys Asn  
 195 200 205  
 Asn Arg Lys Glu Phe Pro Gln Glu Met Leu Arg Met Gly Ile His Ile  
 210 215 220  
 Pro Asp Arg Asp Ala Ala Trp Glu Leu Glu Pro Gly Ala Phe Ser Asp  
 225 230 235 240  
 Leu Tyr Gln Arg Tyr Gln His Cys Asp Ala Pro Ile Cys Pro Tyr Glu  
 245 250 255  
 Gln Gly Arg Asp Ser Phe Glu Asp Glu Gly Arg Trp Cys Leu Ile Leu  
 260 265 270  
 Cys Ala Thr Cys Gly Ser His Gly Thr His Arg Asp Cys Ser Ser Leu  
 275 280 285  
 Arg Phe Asn Ser Lys Lys Trp Glu Cys Glu Glu Cys Ser Pro Ala Ala  
 290 295 300  
 Ala Thr Asp Tyr Ile Pro Glu Asn Ser Gly Asp Ile Pro Cys Cys Ser  
 305 310 315 320  
 Ser Thr Phe His Pro Glu Glu His Phe Cys Arg Asp Asn Thr Leu Glu  
 325 330 335  
 Glu Asn Pro Gly Leu Ser Trp Thr Asp Trp Pro Glu Pro Ser Leu Leu  
 340 345 350  
 Glu Lys Pro Glu Ser Ser Arg Gly Arg Arg Ser Tyr Ser Trp Arg Ser  
 355 360 365  
 Lys Gly Val Arg Ile Thr Asn Ser Cys Lys Lys Ser Lys  
 370 375 380

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

GTCACGTGGA ACCTCTTAAT CTCAGCATCC GGAGCTCCAG GAAGGGAAAA TTTCAAGTCA 60
GATAGAATTC TATATATACC ATTTCTTTGG AACCTTCAGC CCTCAAGATT CCAACATCAT 120
GACCTCAGTT TCAACACAGT TGTCTTAGT CCTCATGTCA CTGCTTTTGG TGCTGCCTGT 180
TGTGGAAGCA GTAGAAGCCG GTGATGCAAT CGCCCTTTTG TTAGGTGTGG TTCTCAGCAT 240
TACAGGCATT TGTGCCTGCT TGGGGGTATA TGCACGAAAA AGAAATGGAC AGATGTGACT 300
TTGAAAGGCC TACTGAGTCA AACCTCACCC TGAAACCTT TGCCTTTAG AGGCTAAACC 360
TGAGATTTGG TGTGTGAAAG GTTCCAAGAA TCAGTAAATA AGGGAGTTTC ACATTTTTC 420
TTGTTTCCAT GAAATGGCAA CAAACATACA TTTATAAATT GAAAAAAAAA TGTTTCTTT 480
ACAACAAATA ATGCACAGAA AAATGCAGCC TATAATTTGC TAGTTAGGTA GTCAAAGAAG 540
TAAGATGGCT GAAATTTACA TAAGTAATAT TTCATAATCT TAGAATTCTC TCAAAGCATG 600
TGAAATAGGA AGAAGGAAGT TCTTGCCCAG AATCTTAGGA AATCACCCT GTTCGGTTAT 660
AATCACTGCC TCCTGAATCG TTGAGGAGTC TTTTAAATTA GATTTTGTG TTGTTGTCTC 720
CCAAGTTAAT ATTATATTTA GATATCAGAG AGTCAGGCAA AAAGGAAAAC TTTTATCTCT 780
AGGGAAAAAA CATTTAGAAA AATGTATTCA GTGTATCTAA TACTGAAATG CGGAAAAAAA 840
TTTAATGTTA AAAAAAACT ATAGACATTG ACATGGAAAA GAGATTTAAT GTTTTGAAAA 900
AAAAACTTTA TATTAAGTGA GTAACATCCT CCTGATGAGA AGTACTATAT TAAATATAAA 960
CCCATTATGT TATAAAAAAA AAAA 984

```

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```

Met Thr Ser Val Ser Thr Gln Leu Ser Leu Val Leu Met Ser Leu Leu
 1 5 10 15
Leu Val Leu Pro Val Val Glu Ala Val Glu Ala Gly Asp Ala Ile Ala
 20 25 30
Leu Leu Leu Gly Val Val Leu Ser Ile Thr Gly Ile Cys Ala Cys Leu
 35 40 45
Gly Val Tyr Ala Arg Lys Arg Asn Gly Gln Met
 50 55

```

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GTTCCTACAG CGGTGAGAGT GAAATGTG

28

- (2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

CCGATACACC AAAGTCTCAT CCCTAAAT

28

- (2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GAGCTAGTGT GAAGGACAAAT AAGCAGAA

28

- (2). INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GTCGCTAACA TCAGAACTAA CAGATTCA

28



(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAGATACTGC AAATGAATTT ACACGGGT

28

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GTCACACTTA ACTCCCATCA CCCGAAAG

28

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCTGAGGCAC TGATCCTTCT GGCAGTTG

28

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TGAGGGCTGA AGGTTCCAAA GAAATGGT

28

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

```

CGCTTTTTTT TTTTTTTTGA CAAGATGGCG GCAGGAGGCA GTGGCGTTGG TGGGAAGCGC 60
AGCTCGAAAA GCGATGCCGA TTCTGGTTTC CTGGGGCTGC GGCCCACTTC GGTGGACCCA 120
GCGCTGAGGC GGCGGCGGCG AGGCCCAAGA AATAAGAAGC GGGGCTGGCG GCGGCTTGCT 180
CAGGAGCCGC TGGGGCTGGA GGTGACCAG TTCCTGGAAG ACGTGC GGCT ACAGGAGCGC 240
ACGAGCGGTG GCTTGTTGTC AGAGGCCCCA AATGAAAAAC TCTTCTTCGT GGACACTGGC 300
TCCAAGGAAA AAGGGCTGAC AAAGAAGAGA ACCAAAGTCC AGAAGAAGTC ACTGCTTCTC 360
AAGAAACCCC TTCGGGTTGA CCTCATCCTC GAGAACACAT CCAAAGTCCC TGCCCCCAAA 420
GACGTCCTCG CCCACCAGGT CCCCACGCC AAGAAGCTCA GGCGGAAGGA GCAGCTATGG 480
GAGAAGCTGG CCAAGCAGGG CGAGCTGCCC CGGGAGGTGC GCAGGGCCCA GGCCCGGCTC 540
CTCAACCCTT CTGCAACAAG GGCCAAGCCC GGGCCCCAGG ACACCGTAGA GCGGCCCTTC 600
TACGACCTCT GGGCCTCAGA CAACCCCCTG GACAGGCCGT TGGTTGGCCA GGATGAGTTT 660
TTCCTGGAGC AGACCAAGAA GAAAGGAGTG AAGCGGCCAG CACGCCTGCA CACCAAGCCG 720
TCCCAGGCGC CCGCCGTGGA GGTGGCGCCT GCCGGAGCTT CCTACAATCC ATCCTTTGAA 780
GACCACCAGA CCCTGCTCTC AGCGGCCAC GAGGTGGAGT TGCAGCGGCA GAAGGAGGCG 840
GAGAAGCTGG AGCGGCAGCT GGCCCTGCCC GCCATGGAGC AGGCCGCCAC CCAGGAGTCC 900
ACATTCCAGG AGCTGTGCGA GGGGCTGCTG GAGGAGTCGG ATGGTGAGGG GGAGCCAGGC 960
CAGGGCGAGG GGCCGGAGGC TGGGGATGCC GAGGTCTGTC CCACGCCCCG CCGCCTGGCC 1020
ACCACAGAGA AGAAGACGGA GCAGCAGCGG CGGCGGGAGA AGGCTGTGCA CAGGCTGCGG 1080
GTACAGCAGG CCGCGTTGCG GGCCGCCCGG CTCCGGCACC AGGAGCTGTT CCGGCTGCGC 1140
GGGATCAAGG CCCAGGTGGC CCTGAGGCTG GCGGAGCTGG CGCGGCGGCG GAGGCGGCGG 1200
CAGGCGCGGC GGGAGGCTGA GGCTGACAAG CCCCGAAGGC TGGGACGGCT CAAGTACCAG 1260
GCACCTGACA TCGACGTGCA GCTGAGCTCG GAGCTGACAG ACTCGCTCAG GACCCTGAAG 1320
CCCGAGGGCA ACATCCTTCG AGACCGGTTT AAGAGCTTCC AGAGGAGGAA TATGATCGAG 1380
CCTCGAGAGA GAGCCAAGTT CAAACGCAAG TACAAGGTGA AGCTGGTGGA GAAGCGGGCG 1440
TTCCGTGAGA TCCAGTTGTA GCTGCCATCA GATGCCGGAG ACTCGCCCTT CAATAAAAAA 1500
TCTCTTCTAG CTGAAAAAAA AAAAAAAA 1528

```

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

```

Met Ala Ala Gly Gly Ser Gly Val Gly Gly Lys Arg Ser Ser Lys Ser
 1 5 10 15
Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr Ser Val Asp Pro
 20 25 30
Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys Lys Arg Gly Trp
 35 40 45

```

Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val Asp Gln Phe Leu  
50 55 60

Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly Leu Leu Ser Glu  
65 70 75 80

Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly Ser Lys Glu Lys  
85 90 95

Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys Ser Leu Leu Leu  
100 105 110

Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn Thr Ser Lys Val  
115 120 125

Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro Asn Ala Lys Lys  
130 135 140

Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala Lys Gln Gly Glu  
145 150 155 160

Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu Leu Asn Pro Ser  
165 170 175

Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val Glu Arg Pro Phe  
180 185 190

Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg Pro Leu Val Gly  
195 200 205

Gln Asp Glu Phe Phe Leu Glu Gln Thr Lys Lys Lys Gly Val Lys Arg  
210 215 220

Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro Ala Val Glu Val  
225 230 235 240

Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu Asp His Gln Thr  
245 250 255

Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg Gln Lys Glu Ala  
260 265 270

Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Met Glu Gln Ala Ala  
275 280 285

Thr Gln Glu Ser Thr Phe Gln Glu Leu Cys Glu Gly Leu Leu Glu Glu  
290 295 300

Ser Asp Gly Glu Gly Glu Pro Gly Gln Gly Glu Gly Pro Glu Ala Gly  
305 310 315 320

Asp Ala Glu Val Cys Pro Thr Pro Ala Arg Leu Ala Thr Thr Glu Lys  
325 330 335

Lys Thr Glu Gln Gln Arg Arg Arg Glu Lys Ala Val His Arg Leu Arg  
340 345 350

Val Gln Gln Ala Ala Leu Arg Ala Ala Arg Leu Arg His Gln Glu Leu  
355 360 365

Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu Arg Leu Ala Glu

|                                                                 |     |         |
|-----------------------------------------------------------------|-----|---------|
| 370                                                             | 375 | 380     |
| Leu Ala Arg Arg Arg Arg Arg Arg Gln Ala Arg Arg Glu Ala Glu Ala |     |         |
| 385                                                             | 390 | 395 400 |
| Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln Ala Pro Asp Ile |     |         |
|                                                                 | 405 | 410 415 |
| Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu Arg Thr Leu Lys |     |         |
|                                                                 | 420 | 425 430 |
| Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser Phe Gln Arg Arg |     |         |
|                                                                 | 435 | 440 445 |
| Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys Arg Lys Tyr Lys |     |         |
|                                                                 | 450 | 455 460 |
| Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile Gln Leu         |     |         |
|                                                                 | 465 | 470 475 |

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

```

ACAAGATGGC GCGCCGAAG GGGAGCCTCT GGGTGAGGAC CCAACTGGGG CTCCCGCCGC 60
TGCTGCTGCT GACCATGGCC TTGGCCGGAG GTTCGGGGAC CGCTTCGGCT GAAGCATTGT 120
ACTCGGTCTT GGGTGATACG GCGTCTTGCC ACCGGGCGCTG TCAGTTGACC TACCCCTTGC 180
ACACCTACCC TAAGGAAGAG GAGTTGTACG CATGTCAGAG AGGTTGCAGG CTGTTTTCAA 240
TTTGTCAGTT TGTGGATGAT GGAATTGACT TAAATCGAAC TAAATTGGAA TGTGAATCTG 300
CATGTACAGA AGCATATTCC CAATCTGATG AGCAATATGC TTGCCATCTT GGTGCCCAGA 360
ATCAGCTGCC ATTCGCTGAA CTGAGACAAG AACAACTTAT GTCCCTGATG CCAAAAATGC 420
ACCTACTCTT TCCTCTAACT CTGGTGAGGT CATCTGGAG TGACATGATG GACTCCGCAC 480
AGAGCTTCAT AACCTCTTCA TGGACTTTT ATCTTCAAGC CGATGACGGA AAAATAGTTA 540
TATTCCAGTC TAAGCCAGAA ATCCAGTACG CACCACATTT GGAGCAGGAG CCTACAAATT 600
TGAGAGAATC ATCTCTAAGC AAAATGTCCT CAGATCTGCA AATGAGAAAT TCACAAGCGC 660
ACAGGAATTT TCTTGAAGAT GGAGAAAGTG ATGGCTTTTT AAGATGCCTC TCTCTTAACT 720
CTGGGTGGAT TTTAACTACA ACTCTTGTC TCTCGGTGAT GGTATTGCTT TGGATTGTGT 780
GTGCAACTGT TGCTACAGCT GTGGAGCAGT ATGTTCCCTC TGAGAAGCTG AGTATCTATG 840
GTGACTTGGA GTTTATGAAT GAACAAAAGC TAAACAGATA TCCAGCTTCT TCTCTTGTTG 900
TTGTTAGATC TAAACTGAA GATCATGAAG AAGCAGGGCC TCTACCTACA AAAGTGAATC 960
TTGCTCATTG TGAAATTTAA GCATTTTCT TTTAAAAGAC AAGTGTAATA GACATCTAAA 1020
ATTCCACTCC TCATAGAGCT- TTTAAATGG TTTTATTGGA TATAGGCCTT AAGAAATCAC 1080
TATAAAATGC AAATAAAGTT ACTCAAATCT GTGAAGACTG TATTTGCTAT AACTTTATTG 1140
GTATTGTTTT TGTAGTAATT TAAGAGGTGG ATGTTTGGGA TTGTATTATT ATTTTACTAA 1200
TATCTGTAGC TATTTTGTTT TTTGCTTTGG TTATTGTTTT TTTCCCTTTT CTTAGCTATG 1260
AGCTGATCAT TGCTCCTTCT CACCTCCTGC CATGATACTG TCAGTTACCT TAGTTAACAA 1320
GCTGAATATT TAGTAGAAAT GATGCTTCTG CTCAGGAATG GCCCACAAAT CTGTAATTTG 1380
AAATTTAGCA GGAAATGACC TTTAATGACA CTACATTTTC AGGAACTGAA ATCATTAATA 1440
TTTTATTGTA ATAATTAATA AAAAAAAAAA AA 1472

```

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```

Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly Leu
 1 5 10 15
Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr
 20 25 30
Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr Ala Ser Cys
 35 40 45
His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu
 50 55 60
Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys
 65 70 75 80
Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys
 85 90 95
Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala
 100 105 110
Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln
 115 120 125
Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu
 130 135 140
Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser
 145 150 155 160
Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys
 165 170 175
Ile Val Ile Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu
 180 185 190
Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser
 195 200 205
Ser Asp Leu Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu
 210 215 220
Asp Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly
 225 230 235 240
Trp Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp
 245 250 255
Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro Ser
 260 265 270

```

Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu Gln Lys  
275 280 285

Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg Ser Lys Thr  
290 295 300

Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys Val Asn Leu Ala  
305 310 315 320

His Ser Glu Ile

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| GTGATTGGTA | CAGTAGGTTT | ATAAACAGAA | GTTTAAACTT | GTAAGCTTAA | GCTTCCGTTT | 60   |
| ATAAACAGAA | GTTTAAAATT | ATAGGTCCTG | TTTAACATTC | AGCTCTGTTA | ACTCACTCAT | 120  |
| CTTTTGTGT  | TTTACACTT  | TGTCAAGATT | TCTTTACATA | TTCATCAATG | TCTGAAGAAG | 180  |
| TTACTTATGC | AGATCTTCAA | TTCCAGAACT | CCAGTGAGAT | GGAAAAAATC | CCAGAAATTG | 240  |
| GCAAATTTGG | GGAAAAAGCA | CCTCCAGCTC | CCTCTCATGT | ATGGCGTCCA | GCAGCCTTGT | 300  |
| TTCTGACTCT | TCTGTGCCTT | CTGTTGCTCA | TTGGATTGGG | AGTCTTGGA  | AGCATGTTTC | 360  |
| ATGTAACCTT | GAAGATAGAA | ATGAAAAAAA | TGAACAACT  | ACAAAACATC | AGTGAAGAGC | 420  |
| TCCAGAGAAA | TATTTCTCTA | CAACTGATGA | GTAACATGAA | TATCTCCAAC | AAGATCAGGA | 480  |
| ACCTCTCCAC | CACACTGCAA | ACAATAGCCA | CCAAATTATG | TCGTGAGCTA | TATAGCAAAG | 540  |
| AACAAGAGCA | CAAATGTAAG | CCTTGTCCTA | GGAGATGGAT | TTGGCATAAG | GACAGCTGTT | 600  |
| ATTTCTTAAG | TGATGATGTC | CAAACATGGC | AGGAGAGTAA | AATGGCCTGT | GCTGCTCAGA | 660  |
| ATGCCAGCCT | GTTGAAGATA | AACAACAAAA | ATGCATTGGA | ATTTATAAAA | TCCCAGAGTA | 720  |
| GATCATATGA | CTATTGGCTG | GGATTATCTC | CTGAAGAAGA | TTCCACTCGT | GGTATGAGAG | 780  |
| TGGATAATAT | AATCCACTCC | TCTGCCTGGG | TTATAAGAAA | CGCACCTGAC | TTAAATAACA | 840  |
| TGTATTGTGG | ATATATAAAT | AGACTATATG | TTCAATATTA | TCACTGCACT | TATAAACAAA | 900  |
| GAATGATATG | TGAGAAGATG | GCCAATCCAG | TGCAGCTTGG | TTCTACATAT | TTTAGGGAGG | 960  |
| CATGAGGCAT | CAATCAAATA | CATTGAAGGA | GTGTAGGGGG | TGGGGGTTCT | AGGCTATAGG | 1020 |
| TAAATTTAAA | TATTTTCTGG | TTGACAATTA | GTTGAGTTTG | TCTGAAGACC | TGGGATTTTA | 1080 |
| TCATGCAGAT | GAAACATCCA | GGTAGACATC | TTCCAGAGAG | ATAGACTGTG | AATGTTAATG | 1140 |
| CCAGAGAGGT | ATAATGAAGC | ATGTCCMACY | TCCCACTTTC | CATCATGGCY | TGAACCYKGG | 1200 |
| RGGAAGAGGA | AGTCCATTCA | GATAGTTGTG | GGGGGCCCTT | GAATTTTCAT | TTTCATWWAC | 1260 |
| GTTCTTCCCC | TTCTGGCCAA | GATTTGCCAG | AGGCAACATC | AAAAACCAGC | AAATTKTAAT | 1320 |
| TTTGTCCCAC | AGSGTTGCTA | GGGTGGCATG | GYTCCCCATT | TSGGGTCCAT | CCTAWACTTC | 1380 |
| CATGGGACTC | CCTATGGCTG | AAGGCCTTAT | GAGTCAAAGG | ACTTATAGCC | AATTGATTGT | 1440 |
| TTTAGGCCAG | GTAAGAATGG | ATATGGACAT | GCATTTATTA | CYTYTTAAAA | TTATTATTTT | 1500 |
| AAGTAAAAGC | CAATAAACAA | AAANGNAAAG | GCAAAAAAAA | AAAAA      | AAAAA      | 1560 |
| AAAAA      | AAA        |            |            |            |            | 1573 |

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ser | Glu | Glu | Val | Thr | Tyr | Ala | Asp | Leu | Gln | Phe | Gln | Asn | Ser | Ser |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Glu | Met | Glu | Lys | Ile | Pro | Glu | Ile | Gly | Lys | Phe | Gly | Glu | Lys | Ala | Pro |  |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Pro | Ala | Pro | Ser | His | Val | Trp | Arg | Pro | Ala | Ala | Leu | Phe | Leu | Thr | Leu |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Leu | Cys | Leu | Leu | Leu | Leu | Ile | Gly | Leu | Gly | Val | Leu | Ala | Ser | Met | Phe |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| His | Val | Thr | Leu | Lys | Ile | Glu | Met | Lys | Lys | Met | Asn | Lys | Leu | Gln | Asn |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |  |
| Ile | Ser | Glu | Glu | Leu | Gln | Arg | Asn | Ile | Ser | Leu | Gln | Leu | Met | Ser | Asn |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Met | Asn | Ile | Ser | Asn | Lys | Ile | Arg | Asn | Leu | Ser | Thr | Thr | Leu | Gln | Thr |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Ile | Ala | Thr | Lys | Leu | Cys | Arg | Glu | Leu | Tyr | Ser | Lys | Glu | Gln | Glu | His |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Lys | Cys | Lys | Pro | Cys | Pro | Arg | Arg | Trp | Ile | Trp | His | Lys | Asp | Ser | Cys |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Tyr | Phe | Leu | Ser | Asp | Asp | Val | Gln | Thr | Trp | Gln | Glu | Ser | Lys | Met | Ala |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Cys | Ala | Ala | Gln | Asn | Ala | Ser | Leu | Leu | Lys | Ile | Asn | Asn | Lys | Asn | Ala |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Leu | Glu | Phe | Ile | Lys | Ser | Gln | Ser | Arg | Ser | Tyr | Asp | Tyr | Trp | Leu | Gly |  |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Leu | Ser | Pro | Glu | Glu | Asp | Ser | Thr | Arg | Gly | Met | Arg | Val | Asp | Asn | Ile |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Ile | His | Ser | Ser | Ala | Trp | Val | Ile | Arg | Asn | Ala | Pro | Asp | Leu | Asn | Asn |  |  |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |  |  |
| Met | Tyr | Cys | Gly | Tyr | Ile | Asn | Arg | Leu | Tyr | Val | Gln | Tyr | Tyr | His | Cys |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Thr | Tyr | Lys | Gln | Arg | Met | Ile | Cys | Glu | Lys | Met | Ala | Asn | Pro | Val | Gln |  |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Leu | Gly | Ser | Thr | Tyr | Phe | Arg | Glu | Ala |     |     |     |     |     |     |     |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     |     |     |  |  |

## (2) INFORMATION FOR SEQ ID NO:189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GAGTTATATG | ACACTCAAAG | GAAAAGCAAA | AGAGCATTAA | GAAGTGTCTG | TTTTTGTTAT | 60  |
| TGCCATTTCA | TAAATATTTT | AGTAGGTGTT | CAATTCATT  | GGATATTCTT | TTTTTTAAT  | 120 |
| TGTCTTTGTA | CCTATGATTG | AAAACAGTAG | TTGGTCTATG | ACTTTTGAGG | AGAGGGAGAA | 180 |
| CCGAAGATTA | CAGGAGGCCA | GCATGAGGTT | GGAACAAGAG | AATGATGACC | TTGCCCATGA | 240 |
| ACTAGTAACA | AGCAAAATTG | CTCTACGGAA | TGACTTGGAT | CAGGCAGAAG | ACAAGGCAGA | 300 |
| TGTGTTGAAT | AAAGAGCTCC | TTTTGACCAA | ACAGAGGCTG | GTGGAGACTG | AAGAGGAGAA | 360 |
| GAGGAAGCAA | GAGGAAGAGA | CTGCCCAGCT | AAAAGAAGTC | TTCAGGAAAC | AGCTAGAGAA | 420 |
| GGCAGAATAT | GAAATAAAGA | AGACTACAGC | TATCATTGCT | GAGTATAAAC | AGGTAATGTA | 480 |
| CTTCTGTGGC | ACATAGAGCT | AGTTATAGTT | TGCTGCTATA | AAAGTAATTT | TTTTTTTTTT | 540 |
| TTGCTTGAGG | CCAGGAGTTT | GAGACTAGCC | TGAGCAACAT | AGCAGGACTC | CGTCCCAAGG | 600 |
| AAAAAAAAAA | AAAAAAAA   |            |            |            |            | 618 |

## (2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

```

Met Ile Glu Asn Ser Ser Trp Ser Met Thr Phe Glu Glu Arg Glu Asn
1 5 10 15
Arg Arg Leu Gln Glu Ala Ser Met Arg Leu Glu Gln Glu Asn Asp Asp
 20 25 30
Leu Ala His Glu Leu Val Thr Ser Lys Ile Ala Leu Arg Asn Asp Leu
 35 40 45
Asp Gln Ala Glu Asp Lys Ala Asp Val Leu Asn Lys Glu Leu Leu Leu
 50 55 60
Thr Lys Gln Arg Leu Val Glu Thr Glu Glu Glu Lys Arg Lys Gln Glu
65 70 75 80
Glu Glu Thr Ala Gln Leu Lys Glu Val Phe Arg Lys Gln Leu Glu Lys
 85 90 95
Ala Glu Tyr Glu Ile Lys Lys Thr Thr Ala Ile Ile Ala Glu Tyr Lys
 100 105 110
Gln Val Met Tyr Phe Cys Gly Thr
 115 120

```

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

```

TGCAGAATCC AGAATGGATG TCCTCTTTGT AGCCATCTTT GCTGTGCCAC TTATCCTGGG 60
ACAAGAATAT GAGGATGAAG AAAGACTGGG AGAGGATGAA TATTATCAGG TGGTCTATTA 120
TTATACAGTC ACCCCAGTT ATGATGACTT TAGTGCAGAT TTCACCATTG ATTACTCCAT 180
ATTTGAGTCA GAGGACAGGC TGAACAGGTT GGATAAGGAC ATAACAGAAG CAATAGAGAC 240
TACCATTAGT CTTGAAACAG CACGTGCAGA CCATCCGAAG CCTGTAAGT TGAAACCAGT 300
AACAACGGAA CCTAGTCCAG ATCTGAACGA TGCCGTGTCC AGTTTGCGAA GTCCTATTCC 360
CCTCCTCCTG TCGTGTGCCT TTGTTCTAGT GGGGATGTAT TTCATGTAGA AGGTGGAAGA 420
AGGCTGCTAT GACTCTTTGG ATGGGAGTCT GGCAAGAGGA AATTGGAAGA TAAAATAAAT 480
AATAAGTGAA ATAAAAAAAA AAAAAAAAAA
 510

```

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:



```

Met Asp Val Leu Phe Val Ala Ile Phe Ala Val Pro Leu Ile Leu Gly
1 5 10 15
Gln Glu Tyr Glu Asp Glu Glu Arg Leu Gly Glu Asp Glu Tyr Tyr Gln
20 25 30
Val Val Tyr Tyr Tyr Thr Val Thr Pro Ser Tyr Asp Asp Phe Ser Ala
35 40 45
Asp Phe Thr Ile Asp Tyr Ser Ile Phe Glu Ser Glu Asp Arg Leu Asn
50 55 60
Arg Leu Asp Lys Asp Ile Thr Glu Ala Ile Glu Thr Thr Ile Ser Leu
65 70 75 80
Glu Thr Ala Arg Ala Asp His Pro Lys Pro Val Thr Val Lys Pro Val
85 90 95
Thr Thr Glu Pro Ser Pro Asp Leu Asn Asp Ala Val Ser Ser Leu Arg
100 105 110
Ser Pro Ile Pro Leu Leu Leu Ser Cys Ala Phe Val Gln Val Gly Met
115 120 125
Tyr Phe Met
130

```

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 883 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```

CATCTGACCA TCCATATCCA ATGTTCTCAT TTAAACATTA CCCAGCATCA TTGTTTATAA 60
TCAGAAACTC TGGTCCTTCT GTCTGGTGGC ACTTAGAGTC TTTTGTGCCA TAATGCAGCA 120
GTATGGAGGG AGGATTTTAT GGAGAAATGG GGATAGTCTT CATGACCACA AATAAATAAA 180
GGAAACTAA GCTGCATTGT GGGTTTTGAA AAGGTTATTA TACTTCTTAA CAATTCCTTT 240
TTTCAGGGAC TTTTCTAGCT GTATGACTGT TACTTGACCT TCTTTGAAAA GCATTCCCAA 300
AATGCTCTAT TTTAGATAGA TTAACATTAA CCAACATAAT TTTTTTTAGA TCGAGTCAGC 360
ATAAATTTCT AAGTCAGCCT CTAGTCGTGG TTCATCTCTT TCACCTGCAT TTTATTTGGT 420
GTTTGTCTGA AGAAAGGAAA GAGGAAAGCA AATACGAATT GTACTATTTG TACCAAATCT 480
TTGGGATTCA TTGGCAAATA ATTTCACTGT GGTGTATTAT TAAATAGAAA AAAAAAATTT 540
TGTTTCCTAG GTTGAAAGGC TAATTGATAC GTTTGACTTA TGATGACCAT TTATGCACTT 600
TCAAATGAAT TTGCTTTCAA AATAAATGAA GAGCAGCTGT CCTTCTTTCC TCTTTAAGT 660
GTTTCAGCTGT GGCATGCTCA GAGGTTCTTG CTGGATTCCA GCTGGAGCGG TGTGATACCC 720
TTCTTTTTC GCTGTTCTGT CCTTCCTTTC TTGTATCCAC CAAAGTGGAG ACAAATACAT 780
GATCTCAAAG ATACACAGTA CCTACTTAAT TCCAGCTGAT GGGAGACCAA AGAATTTGCA 840
AGTGGATGGT TTGGTATCAC TGTAAATAAA AAGAGGGCCT GGG 883

```

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 79 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Met Met Thr Ile Tyr Ala Leu Ser Asn Glu Phe Ala Phe Lys Ile Asn

|                                                                 |    |    |    |
|-----------------------------------------------------------------|----|----|----|
| 1                                                               | 5  | 10 | 15 |
| Glu Glu Gln Leu Ser Phe Phe Pro Leu Leu Ser Val Gln Leu Trp His |    |    |    |
|                                                                 | 20 | 25 | 30 |
| Ala Gln Arg Phe Leu Leu Asp Ser Ser Trp Ser Gly Val Ile Pro Phe |    |    |    |
|                                                                 | 35 | 40 | 45 |
| Phe Phe Ser Cys Ser Cys Leu Pro Phe Leu Tyr Pro Pro Lys Trp Arg |    |    |    |
|                                                                 | 50 | 55 | 60 |
| Gln Ile His Asp Leu Lys Asp Thr Gln Tyr Leu Leu Asn Ser Ser     |    |    |    |
| 65                                                              | 70 | 75 |    |

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 110 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 60  |
| AAAAAAAAAA AAAAAAAAAAGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA          | 110 |

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 861 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TAGGCCTCTT TGGCCGGTGC TGCCTGAGAA GGATTGGCAC GGGCACAGAC CACTGCCCCC  | 60  |
| ACCTGCCCTG CGCCATCTAC CCAAGAAGGC TCGGCACGGG CACCAACCAC TGCCTCCAAC  | 120 |
| TGCCCCATGC TGCCTGAGAA GGCACCTGCAC GGCCACCCCG AACTGCCCCG CACTGTCCCT | 180 |
| ACCCGGGCGAG CCATGCGAGC GGCTGGAAC TGTGCTGGCCT TCTGCTGCCT GGTCTTGAGC | 240 |
| ACCACTGGGG GCCCTTCCCC AGATACTTGT TCCCAGGACC TTAACCTACG TGTGAAGCCA  | 300 |
| GGATTTCTTA AAACAATAAA GACCAATGAC CCAGGAGTCC TCCAAGCAGC CAGATACAGT  | 360 |
| GTTGAAAAGT TCAACAACCTG CACGAACGAC ATGTTCTTGT TCAAGGAGTC CCGCATCACA | 420 |
| AGGGCCCTAG TTCAGATAGT GAAAGGCCTG AAATATATGC TCGARGTGGA AATTGGCAGA  | 480 |
| ACTACCTGCA AGAAAAACCA GCACCTGCGT CTGGATGACT GTGACTTCCA AACCAACCAC  | 540 |
| ACCTTGAAGC AGACTCTGAG CTGCTACTCT GAAGTCTGGG TCGTGCCCTG GCTCCAGCAC  | 600 |
| TTCGAGGTGC CTGTTCTCCG TTGTCACCTG CCCCCGCTC TTCAGCAAGA CCACAGCCAT   | 660 |
| GACAAACACC AGGATGCATG CTCCTTGTC CCTCCCACCC GCYWSRTGAC CRRRCCTSAC   | 720 |
| AGACCCTCTC RGGCCTCWGA CGAGTGAGCG GRTGAAGTGC MAYTGGGTSA CMGCAGGGCA  | 780 |
| GCTRGAATGG CAGCWTGGTA GCGCCTCCTA ACAGRTTAAA TRGATCACAT GTGTTTCTAA  | 840 |
| AATTAAAAA AAAAAAAAAA A                                             | 861 |

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 167 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Pro | Glu | Lys | Ala | Leu | His | Gly | His | Pro | Gln | Leu | Pro | Arg | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Pro | Thr | Arg | Ala | Ala | Met | Arg | Ala | Ala | Gly | Thr | Leu | Leu | Ala | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Cys | Leu | Val | Leu | Ser | Thr | Thr | Gly | Gly | Pro | Ser | Pro | Asp | Thr | Cys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Gln | Asp | Leu | Asn | Ser | Arg | Val | Lys | Pro | Gly | Phe | Pro | Lys | Thr | Ile |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Lys | Thr | Asn | Asp | Pro | Gly | Val | Leu | Gln | Ala | Ala | Arg | Tyr | Ser | Val | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Phe | Asn | Asn | Cys | Thr | Asn | Asp | Met | Phe | Leu | Phe | Lys | Glu | Ser | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Thr | Arg | Ala | Leu | Val | Gln | Ile | Val | Lys | Gly | Leu | Lys | Tyr | Met | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Val | Glu | Ile | Gly | Arg | Thr | Thr | Cys | Lys | Lys | Asn | Gln | His | Leu | Arg |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Leu | Asp | Asp | Cys | Asp | Phe | Gln | Thr | Asn | His | Thr | Leu | Lys | Gln | Thr | Leu |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Ser | Cys | Tyr | Ser | Glu | Val | Trp | Val | Val | Pro | Trp | Leu | Gln | His | Phe | Glu |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Val | Pro | Val | Leu | Arg | Cys | His |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

ANCCAGAATC GGCATCGCTT TTCGAGCTG

29

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

TNTGGTGCGT ACTGGATTTC TGGCTTAGA

29

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GNTAACAGAG CTGAATGTTA AACAGGACC

29

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TNTCCTCAAA AGTCATAGAC CAACTACTG

29

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

GNTCAGCCTG TCCTCTGACT CAAATATGG

29

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TNACCTGCAT TTTATTTGGT GTTGTCTG

29

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TNAACACTGT ATCTGGCTGC TTGGAGGAC

29

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2556 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

|                                                                     |      |
|---------------------------------------------------------------------|------|
| GCAAGATTTG GCCTGGATTC TTCTGAGGAT GTGAAGTAAT GGAAACAGTA AGACTGTTCC   | 60   |
| AGACTAGGGG AAGACTAGAG ACCTAATAGC TGGATTCCAT GTGATCTTTT GTTGGACTTT   | 120  |
| GGGATTGGAG GTGAGAGTAG AGAAGGCATA ATGCACGTTT TTGAGACGAG GGAAATGTGA   | 180  |
| ATATAGCCTG TATGCCTACA CTCAAGTCTG AAGACATGTW AACCATGTCT ATACTAACCA   | 240  |
| GCCAAATATT TGAACACTAA AAGGAAGAAT TTTCTTAATG TGGTAATGGT WTCATGGTTG   | 300  |
| TATAGAATGT TCCTCCTCTT GGGAGATGTG TGTTGAAAAT AGGGTTTGAC GTCTAAACCT   | 360  |
| ATTTTGT TTTT GGCAAAAAGG ACGTGTGTCT GTACAAAAGA AGTGGAGCCA GTATGGCAAA | 420  |
| ATGTTTACMA GGACTCTGGG TGAGARGTWC ATAGGTGCTT ACTATACTGT TTTGTTTCTG   | 480  |
| AATTTGGAAT TTCTCAAAAT TAAAAAATA TCTACTGAGG AGCTTTTCGT TTAACTGGT     | 540  |
| GGGGAATGGG TTCTGGGTGG TTTTGCCCCCT TTTCTTTTGA GATTCAAGAA ATCCATGGTG  | 600  |
| AAAGGTTTGG ATTCTATGA AGAAAAGGAG GATAAAGTGA TCAAGGAGAT GGCAGCTCAG    | 660  |
| ATCCGTGAGG TGGAGCAGAG CCGACAGGAG GTGGTTCGGT CTGTCTTAGA GGTGGTTTC    | 720  |
| CCTCGGAGGA TCCAGACCAC CTCAGGCAGT GCCAGACCCA GAAGAGGGCT CTTCAGCACC   | 780  |
| TAGAAGCTGG AAAGGGATGA ACAGGTAAGA CTATTAGGGA ATCTCTTGTT GGAATTTGA    | 840  |
| CATCTTAGAA CATTCTGCAA CCTTTTGCCT GGGAAATGGA AACAGATCTA ATCTTTACCA   | 900  |
| CCCTCATGGC TCAAGGACCT CATCTGGCAG CCTGGCTCAT GTTTTTCAGC CAAGTAGCTT   | 960  |
| CCAGCTTACA GCAGCCCTCA AATTGGACC TGCCACCAGC TCCAGAGCTT GACTGGATGG    | 1020 |
| AGACAGGACC ATCTCTGACA TTCATTGGCC ATCAGGTACA AAGGATAAGC AAGCCAGAAG   | 1080 |
| AGGGCCAATG GTCCCTCAGG TCTCAGGACC CCTTTCTCCT GATTTTCTAC CTATTCAAGC   | 1140 |
| CACTGCTGCC TCCACTGCAG GCTTTTCCTT CTTCTTCAC TGTTCCCTAG TAGTGTTC      | 1200 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| AGACCTCTTC TCACCCTCCA AAGCGATCCT ATTCACATGT ATTGACACTT AGGAGTGCCA | 1260 |
| ACTCCTAAAT CTTGCCCTCT GTAGAACTCA TAGTTCCAAC TCAACACAGG ACATTAAATA | 1320 |
| TCCCACAGGC ATCTGAAACT AACCCCCACC ACTCCTATAT TTCCAATCAC TAGATGCAGA | 1380 |
| TCCTTTCTTT TTCCATCTCC CATATCCTGT CAACAAGCGG TCAATTTTAA CCTGTCTGCC | 1440 |
| TCCATTGAGC CTTTGGGCAA TTTCTACTCC CCCTTCAATC CTGCCTCACA AACAGAAAAT | 1500 |
| CATTGTACCA CTTATGATTT TACTCTACAC TTCAGCTGTA TTGTGTTGCT TCGGGCTTTT | 1560 |
| GCAGTTGCCA TTGTCTAAAA CATGCTTTCC TTCCCTCATC ACCTAGTTTA CCTTCAACTG | 1620 |
| TTAGCTCAAA TGTCACCTTT TCATAAAAGG CTTATCTGAA CAGGTTATCT CTATTTCAAG | 1680 |
| TGGATGTAGC ACCATGTAAA GTTGCAAATG TAATTTACGT AACTTGTGCT TAATGCTCTT | 1740 |
| CCCCAATTAT ATGTATGCTG TGAGGGCAAG GTTTTGCTCC CCTGGCATGT AATAGCCACT | 1800 |
| CTACTTACAG ACATCTCCAC TGTTATGACT GTGAGCTTCC TGAGGACAGG GTTGTCTTAG | 1860 |
| AGTGACTTAC TGTGCTTTCA AAGTTTAACA TCAGCTGGGG TGCAGAATTA GCATTGTGGC | 1920 |
| AGCAGTCACA CCCACCTCTT TTAAAGTGTG CTTTGTCTAT CGTTTCTAGG ATTTTTTTTT | 1980 |
| TTAATCATGC CTAGACTTTA ACTAGCACTT TTTTCCCAT TTCCAACCTAC AGGATATACC | 2040 |
| AGGAGTTGGT AACATCCACT CAGGTGCCAC ACCTCCCTGG ATGATCCAAG ATGAAGAATA | 2100 |
| CATTGCTGGG AACCAAGAAA TAGGACCATC CTATGAAGAA TTTCTTAAAG AAAAGGAAAA | 2160 |
| ACAGAAGTTG AAAAACTCC CCCCAGACCG AGTTGGGGCC AACTTTGATC ACAGCTCCAG  | 2220 |
| GACCAGTGCA GGCTGGCTGC CCTCTTTTGG CCGTGTCTGG AATAATGGAC GCCGCTGGCA | 2280 |
| GTCCAGACAT CAATTCAAAA CTGAAGCTGC AGCAATGAAG AAGCAGTCAC ATACAGAAAA | 2340 |
| AAGCTAATCA TGCTCTCTAC CAACTACCAT GAGGCTAAAA GCAAAGTCAA CAAACCCCTA | 2400 |
| TTATACCTTC CACCAAATTC TTTATCATG TCTTTCTTAG GAAACAGACA TACTCATTCA  | 2460 |
| TTTGATTTAA TAAAGTTTAA TTTTCCAAA TGTACAGCTG GTTGGACCTG TAAAAAATAA  | 2520 |
| TTAAAGAAT CAGAACCATA AAAAAAAAAA AAAAAA                            | 2556 |

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Thr | Asp | Leu | Ile | Phe | Thr | Thr | Leu | Met | Ala | Gln | Gly | Pro | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Leu Ala Ala Trp Leu Met Phe Phe Ser Gln Val Ala Ser Ser Leu Gln  
                     20                                    25                                    30  
 Gln Pro Ser Asn Leu Asp Leu Pro Pro Ala Pro Glu Leu Asp Trp Met  
                     35                                    40                                    45  
 Glu Thr Gly Pro Ser Leu Thr Phe Ile Gly His Gln Val Gln Arg Ile  
                     50                                    55                                    60  
 Ser Lys Pro Glu Glu Gly Gln Trp Ser Leu Arg Ser Gln Asp Pro Phe  
                     65                                    70                                    75                                    80  
 Leu Leu Ile Phe Tyr Leu Phe Lys Pro Leu Leu Pro Pro Leu Gln Ala  
                     85                                    90                                    95  
 Phe Pro Ser Ser Phe Thr Val Pro  
                     100

## (2) INFORMATION FOR SEQ ID NO:207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| TTCATCTTCT CCCTGTA ACT GAGATTTCTA CCACACCTTT GAACAATGTT CTTTCCCTTC   | 60  |
| TGGTTATCTG AAGACTGTCC TGAAAGGAAG ACATAAGTGT TGTGATTAGT AGAAGCTTTC    | 120 |
| TAGTAGACCA TATTTCTTCT GGATTGTAAT AAAATTGTGA GTAGCTCCTT TTA CTTTGTGTT | 180 |
| CCTGTCTCTG GAAAGCCATT TTTGAATTGC TGATTACTTT GGCTTTAATC AGTGGTCACC    | 240 |
| TAGAAAAAGC TTTGTAATCA TAACACAATG AGTAATTCTT GATAAAAGTT CAGATACAAA    | 300 |
| AGGAGCACTG TAAAACTGGT AGGAGCTATG GTTTAAGAGC ATTGGAAGTA GTTACA ACTC   | 360 |
| AAGGATTTTG GTAGAAAGGT ATGAGTTTGG TCGAAAAATT AAAATAGTGG CAAAATAAGA    | 420 |
| TTTAGTTGTG TTTTCTCAGA GCCGCCACAA GATTGAACAA AATGTTTTCT GTTTGGGCAT    | 480 |
| CCTGAGGAAG TTGTATTAGC TGTTAATGCT CTGTGAGTTT AGAAAAAGTC TTGATAGTAA    | 540 |
| ATCTAGTTTT TGACACAGTG CATGAACTAA GTAGTTAAAT ATTTACATAT TCAGAAAGGA    | 600 |
| ATAGTGGAAA AGGTATCTTG GTTATGACAA AGTCATTACA AATGTGACTA AGTCATTACA    | 660 |
| AATGTGACTG AGTCATTACA GTGGACCCTC TGGGTGCATT GAAAAGAATC CGTTTTATAT    | 720 |
| CCAGGTTTCA GAGGACCTGG AATAATAATA AGCTTTGGAT TTTGCATTCA GTGTAGTTGG    | 780 |
| ATTTTGGGAC CTTGGCCTCA GTGTTATTTA CTGGGATTGG CATACGTGTT CACAGGCAGA    | 840 |
| GTAGTTGATC TCACACAACG GGTGATCTCA CAAAAGTGGT AAGTTTCTTA TGCTCATGAG    | 900 |

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CCCTCCCTTT TTTTTTTTAA TTTGGTGCCT GCAACTTTCT TAACAATGAT TCTACTTCCT 960
GGGCTATCAC ATTATAATGC TCTTGGCCTC TTTTTTGCTG CTGTTTTGCT ATTCTTAAAC 1020
TTAGGCCAAG TACCAATGTT GGCTGTTAGA AGGGATTCTG TTCATTCAAC ATGCAACTTT 1080
AGGGAATGGA AGTAAGTTCA TTTTAAAGTT GTGTTGTCAG TAGGTGCGGT GTCTAGGGTA 1140
GTGAATCCTG TAAGTTCAAA TTTATGATTA GGTGACGAGT TGACATTGAG ATTGTCCTTT 1200
TCCCTGATCA AAAAATGAAT AAAGCCTTTT TAAACAAAAA AAAAAAAAAA AAAAAAAAAA 1260
AAAAAAAAAA AAAAAA 1276

```

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```

Met Ile Leu Leu Pro Gly Leu Ser His Tyr Asn Ala Leu Gly Leu Phe
1 5 10 15

Phe Ala Ala Val Leu Leu Phe Leu Asn Leu Gly Gln Val Pro Met Leu
 20 25 30

Ala Val Arg Arg Asp Ser Val His Ser Thr Cys Asn Phe Arg Glu Trp
35 40 45

Lys

```

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```

GGGGCTCGTC TGTTCCAGGA GCCCTGAACC AAAGAGCAGC GGAGTTTGAG AAGCCAGCAG 60
CTCGGGGTTC GGCAGCAGCG GTCCCATCGG CTGAAGTTTC GGGGGGGTGG GGCGCCGAGC 120
GCGCGGGGTG GGGGGGGTCC TGGTCTTTGG CTTCTCGACT CGGTCCTGTT TCGACAGCGA 180
ACATGTCGCG GCCTGTCAGA AATAGGAAGG TTGTTGATTA CTCACAGTTT CAGGAATCTG 240
ATGATGCAGA TGAAGATTAT GGAAGAGATT CGGGCCCTCC CACTAAGAAA ATTCGATCAT 300
CTCCCCGAGA AGCTAAAAAT AAGAGGCGAT CTGGAAAGAA TTCACAGGAA GATAGTGAGG 360

```



ACTCAGAAGA CAAAGATGTG AAGACCAAGA AGGATGATTC TCACTCAGCA GAGGATAGTG 420  
AAGATGAAAA AGAAGATCAT AAAAATGTGC GCCAACAACG GCAGGCGGCA TCTAAAGCAG 480  
CTTCTAAACA GAGAGAGATG CTCATGGAAG ATGTGGGCAG TGAGGAAGAA CAAGAAGAGG 540  
AGGATGAGGC ACCATTCCAG GAGAAAGATT CCGGCAGCGA TGAAGATTTT CTAATGGAAG 600  
ATGATGACGA TAGTGACTAT GGCAGTTCGA AAAAGAAAAA CAAAAAGATG GTTAAGAAGT 660  
CCAAACCTGA AAGAAAAGAA AAGAAAATGC CCAAACCCAG ACTAAAGGCT ACAGTGACGC 720  
CAAGTCCAGT GAAAGGCAAA GGGAAAGTGG GTCGCCCCAC AGCTTCAAAG GCATCAAAGG 780  
AAAAGACTCC TTCTCCCAAA GAAGAAGATG AGGAACCGGA AAGCCCGCCA GAAAAGAAAA 840  
CATCTACAAG CCCCCACCC GAGAAATCTG GGGATGAAGG GTCTGAAGAT GAAGCCCCTT 900  
CTGGGGAGGA TTAAAAGTGA TGATGGTCTG GGGAGAGATT TTATTAAAAA AAAAAAGAAA 960  
AAAAAAGAAA AAAGAGGGAG GAAAAAAAG AACCTACTTA AGATAGAACA TGGTTTTGGC 1020  
TATGGCTTGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1080  
AAAAAAAAAA AAAAAAAAAA AAAAAAAA 1108

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Met Ser Arg Pro Val Arg Asn Arg Lys Val Val Asp Tyr Ser Gln Phe  
1 5 10 15  
Gln Glu Ser Asp Asp Ala Asp Glu Asp Tyr Gly Arg Asp Ser Gly Pro  
20 25 30  
Pro Thr Lys Lys Ile Arg Ser Ser Pro Arg Glu Ala Lys Asn Lys Arg  
35 40 45  
Arg Ser Gly Lys Asn Ser Gln Glu Asp Ser Glu Asp Ser Glu Asp Lys  
50 55 60  
Asp Val Lys Thr Lys Lys Asp Asp Ser His Ser Ala Glu Asp Ser Glu  
65 70 75 80  
Asp Glu Lys Glu Asp His Lys Asn Val Arg Gln Gln Arg Gln Ala Ala  
85 90 95  
Ser Lys Ala Ala Ser Lys Gln Arg Glu Met Leu Met Glu Asp Val Gly  
100 105 110  
Ser Glu Glu Glu Gln Glu Glu Glu Asp Glu Ala Pro Phe Gln Glu Lys  
115 120 125

Asp Ser Gly Ser Asp Glu Asp Phe Leu Met Glu Asp Asp Asp Ser  
 130 135 140

Asp Tyr Gly Ser Ser Lys Lys Lys Asn Lys Lys Met Val Lys Lys Ser  
 145 150 155 160

Lys Pro Glu Arg Lys Glu Lys Lys Met Pro Lys Pro Arg Leu Lys Ala  
 165 170 175

Thr Val Thr Pro Ser Pro Val Lys Gly Lys Gly Lys Val Gly Arg Pro  
 180 185 190

Thr Ala Ser Lys Ala Ser Lys Glu Lys Thr Pro Ser Pro Lys Glu Glu  
 195 200 205

Asp Glu Glu Pro Glu Ser Pro Pro Glu Lys Lys Thr Ser Thr Ser Pro  
 210 215 220

Pro Pro Glu Lys Ser Gly Asp Glu Gly Ser Glu Asp Glu Ala Pro Ser  
 225 230 235 240

Gly Glu Asp

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2952 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ASTTCRAATT CGGCCTTCAT GGMCTAGCAC GGACTCTGCC TTCTAAAAGT GGAACCCCMC | 60  |
| AGTMCCAGCT GTTGCCTMAG SGTGGACASA TCAGSCGAAG CTCCTGCCCT GCCTGTTGGC | 120 |
| AGCMTCCATG GGCCAAGCTC TTGCCTCTCA CCATCCTCTC CAGGCCCAGT ACTGTTTCCA | 180 |
| GCCGGCCTCT CCAGGCCCAA CTCTCCCTCT CAGCTGTGCC TGCCGGCCCA GCTCCTACCT | 240 |
| CGCAAAGCC ACGTTCGGCC CAGCTCCTGC CCAGCTCCTG GCAGCCTTTG TAAACCCAG   | 300 |
| GATCCTCTAA GTCAGGCCTT TCAGGCCCTG CCTTTGGCTC CCCGGTGGCA TGGAGAGGCC | 360 |
| CAGCTCCTGC CTGACAGCGG CCTCTCCAGG CCCAGCTCTT GCCTCACGTT GGCTCCCTG  | 420 |
| GGCCACGTTT CCGCCTGCCT CGCGGCAGCC CCGACAATCC CGGCTCCTGC CTCCCGATGG | 480 |
| CATCTTTAGG CTCATCTCGT GCCTCACCAC GGCCTGCACC AGGCCACACT CCTGCCTTTC | 540 |
| GGTGGCCTCC GCGGGCCTGA CTCCTGCGTC CCAATGGCCT CTTTAGGCCC GGCTCGTGCC | 600 |
| TCGCCGCGGC CTCCTGAGGC CCACCTTTGC CTTTCTGGCA GCCTCTCCAG GCCCAGGACT | 660 |
| TCCTCAAGTC GGCCTCTGCC AGCCCAGTGG CCGCCTCCCG GCCTCCTCTC CGGGCCCAGC | 720 |

|            |            |             |             |             |            |      |
|------------|------------|-------------|-------------|-------------|------------|------|
| TCCTTGCTCG | TGGCTGCGCC | CGCGGGCCCCA | GCTCCTGCCT  | CTGAACATCC  | TCCTGTGACT | 780  |
| CGGCTCCTGC | CCAGCTCCCA | GCGGCCTCCG  | TAGACCCGAA  | GCCTCCTCCG  | GTCCAGCTCT | 840  |
| CCAGGCCTGC | CTCCTGCCTC | GTGGCGGCCT  | TCCCCGGCCA  | TGCTCGTGCC  | GGCTTCCCGG | 900  |
| CAGCCTCCAC | GAGCCCGGCT | CCTGCCTCAC  | GCGGGCCCCCT | CCAGGCCCCAG | CTCGTGCCTC | 960  |
| GCGGCGGCCT | CTCCAGGCCC | GGCTCCCGCC  | CAGCCCGACG  | GCGTCTCCCA  | GCCCAAGGCT | 1020 |
| CCCTTCCTCA | ACGTCGGCCC | CTCTGGGCCC  | AGCTCCTGCC  | TCCCGCTGAT  | GGCCTGTGCG | 1080 |
| GGCCACCCG  | AGGCGGCCCC | AAGTCGGCCT  | CGCCAGGCCC  | AGCTCCTGCC  | TGGCGTAGGC | 1140 |
| CCCTGGGGGC | ACGGCCTCTG | CCCMACAGTG  | GCCCCCTCCG  | GCCCAGCTCG  | TGCCTCGGCT | 1200 |
| TGGCCGCTC  | AGGCCAGCT  | CCTGCCTGTG  | GGCGGCCTCT  | CTCCAGACCC  | GGCTCTCGCC | 1260 |
| TCCCGGCATC | CTCTCCAGGC | CCAGAGCTGT  | TTCCAGTTGC  | TAGACCATTT  | TTGTGCCTGC | 1320 |
| CTCGTTGCAG | CATCTCCAAG | CCCAGCTTTT  | GCTTTTCTGC  | AGTTTCTTGA  | GGCCGAAGTC | 1380 |
| CATTTTTCGA | ATGGCTTATT | TAGGCCCAGC  | TCTTGCGTTT  | GCATTGTCCC  | TTCAGGCCCA | 1440 |
| GAAGTTTCTC | ACGTCATCGT | CACCAGGCCT  | AGCTTCTGCA  | TCTGGTCAGC  | CTTTTAAGGC | 1500 |
| CCAGCTTTTG | CCTCATAAAC | TCAGCTCCTG  | TTAATGGCG   | GCCTCCCAGG  | TCCCACCTTC | 1560 |
| TGCCTTCCTG | TGTCCACTCC | AGGCCCAGCT  | ACTGCCTTGG  | TGCTCTTTTT  | AAGTCAATAA | 1620 |
| TTTTTTCCAG | TCGACCTCTC | CAGGCCCAAC  | TTGTACCTCT  | GAGTGTCTCT  | TAGGATCTCA | 1680 |
| GCTTCTGCCT | AACAATGACC | TCTTTAGACT  | CAGCTCATTT  | TCACTGCTAC  | ATCTTCAAGC | 1740 |
| CATTCTCCTG | CCTCTTGGA  | ACCTCTAGTG  | GCCCAGCTTC  | TGCCTCACAG  | CAGCCTCTCC | 1800 |
| ATGCATGCCT | AGCTCCTGCC | TCTTTAGGGA  | ACTTACAGGC  | CTAAAGCTTT  | CTTAATTTGG | 1860 |
| GCTTCTCAAG | CCCAGCTCCT | GCCTTCTGTT  | GGGCTCTACA  | GGCCTGGCAT  | CATCCTTTCA | 1920 |
| ACAGCCTCTT | TAGGCCCGGC | CTCTCCAGGA  | CCAAAACATC  | CTTAAGTCAA  | CCTCACCAGG | 1980 |
| CCCGGCTCCT | GTCTCCTTGC | GGCCTCCAGA  | GGCCGAGCTT  | TTGCCTGCCA  | ATGGCCTCTC | 2040 |
| TAGCCCCAGC | TTTTGCCTGC | CAATGGCCTC  | TCTAGCCCCA  | GCTTCTGCCT  | TTCATCGGTC | 2100 |
| TCTCCAGGCT | TAGCTCCTTT | CTCTTCACGG  | CCTCTGCAGG  | CCTAAAGCTT  | CCTCAATTTG | 2160 |
| GCATCTCCAG | GCCCAGCTCC | TGCCTCCAGG  | CCGCCTCTGC  | AGGCCTATCT  | CAAGCCTTAC | 2220 |
| AACAGCCTCT | TTACCCCCAG | CTCCTTTCTC  | CGACTTGTCT  | CTCCAGGCCT  | AGAACTTCCT | 2280 |
| CATGTTTACC | TCACCAGGCC | CACCTCCTGC  | CTTCCAGTAG  | CGTCTACAAG  | TTTGGCTCCT | 2340 |
| GCCTCCCATG | GATCTCTCCA | GGCCCCAAAC  | TTTCTCAAGT  | CAACCTCACC  | AGGCCCGGCT | 2400 |
| TCTCCCTTTC | ATCAGCCTTC | CAAAGGCCAG  | CTTTTGCTTC  | ATGTCTGCCT  | TCCGAGTCCC | 2460 |
| AGCTCCTGTT | TTATGGCAGC | CTCCTGAGGC  | CCAGCTCCTG  | CCTCCTAGTG  | GCCTCTTTTG | 2520 |
| GCCCAACTCT | TTCCTACCA  | GGGCCTTCCA  | GACCACGTTC  | CTGCCTTTTA  | GCAGCCACTA | 2580 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| CAGGCCCAGC TTTGCGTCCT TTCAAGAGTC CTGCCTCACA GTGGCCTCCC AAGGGCAACT  | 2640 |
| TTCTGCCTCA TGTCAGCCTC TTGTGCCCTG GTCCTGCTTC CTGGTAGACT CTGCAGGCCC  | 2700 |
| TGCTCCTGCC TTACGTTGCC CCTTTTATAA AGATCCAGTT CCTGCCTCCT GGCTGCCTCT  | 2760 |
| ATGAGCCCCAA ATCCTGCCTA ACAACAACCT GTTTTTGCCC AGCTCCTGCT TCCTGGCAGC | 2820 |
| CTCCTTAGGC CAAAAATTTT CTTCAAGTTGA CCTCTCCAGG CCCAGCTCCT GCCTCTCAGC | 2880 |
| ACCCTCTTTA GGCCCAGCTC CTGCCTTAAT AAATTTGAAT AAATTATTGT TATGTGAAAA  | 2940 |
| AAAAAAAAAA AA                                                      | 2952 |

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 73 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Tyr | Leu | Gly | Pro | Ala | Leu | Ala | Phe | Ala | Leu | Ser | Leu | Gln | Ala |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gln | Asn | Phe | Leu | Thr | Ser | Ser | Ser | Pro | Gly | Leu | Ala | Ser | Ala | Ser | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gln | Pro | Phe | Lys | Ala | Gln | Leu | Leu | Pro | His | Lys | Leu | Ser | Ser | Cys | Leu |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Met | Ala | Ala | Ser | Gln | Val | Pro | Pro | Ser | Ala | Phe | Leu | Cys | Pro | Leu | Gln |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |
| Ala | Gln | Leu | Leu | Pro | Trp | Cys | Ser | Phe |     |     |     |     |     |     |     |  |
|     |     |     | 65  |     |     |     | 70  |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1294 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GTGCCCCGCC GCTGCTGTCA CCCCCGGCCG CTGCTGCCCT CCCC GCCGAG GTTCTACTGC | 60  |
| TCTCCTTCTT AAGAAGGGTG GGAGGCACTC GGTCTCTCCC CACACCTCTC GCCTGAGGCC  | 120 |
| AGGCGCCAGG TGTCGCCTGA AGCCAGACAG CCGGTTTGGG AGCGAGCCTG AGGTCAACCA  | 180 |
| ATCAATGGCT CAGACAGATA AGCCAACATG CATCCC GCCG GAGCTGCCGA AAATGCTGAA | 240 |

GGAGTTTGCC AAAGCCGCCA TTCGGGCGCA GCCGCAGGAC CTCATCCAGT GGGGGGCCGA 300  
 TTATTTTGAG GCCCTGTCCC GTGGAGAGAC GCCTCCGGTG AGAGAGCGGT CTGAGCGAGT 360  
 CGCTTTGTGT AACTGGGCAG AGCTAACACC TGAGCTGTTA AAGATCCTGC ATTCTCAGGT 420  
 TGCTGGCAGA CTGATCATCC GTGCAGAGGA GCTGGCCCAG ATGTGGAAAG TGGTGAATCT 480  
 CCCAACAGAT CTGTTTAATA GTGTGATGAA TGTGGGTCGC TTCACGGAGG AGATCGAGTG 540  
 GCTGAAGTTT TTAGCCCTTG CTTGCAGCGC TCTGGGAGTT GTAAGTTAGC TTGACTGTTT 600  
 TTTGTTCTTG AAGGGGAAAT CTCCCTCTGG GCCTGGAAGG GCAGTGCATC TATACACGCG 660  
 GTCAACTCTG CAGGGCTGAT GATAAACATG CCTCTTCTCC TATTGTCCTT CTCCTCTCTA 720  
 AAGCAAGGTC ATTTCTGTGC TCGTCAGGCA GTGGCAGGGG TTGGGAGGAG GAGAGAGGGA 780  
 AACACTGTGG TCAGGCTCTG GGGAGAGTTG ACTACAGTGT AGCTCTTGGA TTATTTATGA 840  
 ATATTGCCCT CAGATTTATT TTCACTCTGC TCCTTCCATT CATATTCCCA GAGACAACCA 900  
 AGAGCCGACT GTAGAAAAAG ACTTCCAGAC ACCTAGAATA TATATCAATA GACTACTGTTT 960  
 AAAAGGGGTA CAATCTTATA GAAAACTATG TAATAAACAG AATTGGATGC AGAACTCAGA 1020  
 CATAAGAAAG CAAAAACAAA GAGAGATGAG GCTATTTCTG AATTTAGTCA TGACATCTCC 1080  
 ATGGATACAG GATGTTTATA CAGATTTATG CCTTTTCCAA ATTTGACTTG TTTGATATTG 1140  
 GAAAAACAAT TTTACTGTTT TGAAGCCAAA GATGTTGAAA TCAGTTTATA TGTATAGATA 1200  
 TTAAAGCTT GGGTATCTTA TATGTGGACT TACATTGTTA AACATTGTTA AAATAAAATG 1260  
 AATCAAAAAC ATGGTTTTTA AAAAAAAAAA AAAA 1294

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Met Ala Gln Thr Asp Lys Pro Thr Cys Ile Pro Pro Glu Leu Pro Lys  
 1 5 10 15  
 Met Leu Lys Glu Phe Ala Lys Ala Ala Ile Arg Ala Gln Pro Gln Asp  
 20 25 30  
 Leu Ile Gln Trp Gly Ala Asp Tyr Phe Glu Ala Leu Ser Arg Gly Glu  
 35 40 45  
 Thr Pro Pro Val Arg Glu Arg Ser Glu Arg Val Ala Leu Cys Asn Trp  
 50 55 60

Ala Glu Leu Thr Pro Glu Leu Leu Lys Ile Leu His Ser Gln Val Ala  
65 70 75 80

Gly Arg Leu Ile Ile Arg Ala Glu Glu Leu Ala Gln Met Trp Lys Val  
85 90 95

Val Asn Leu Pro Thr Asp Leu Phe Asn Ser Val Met Asn Val Gly Arg  
100 105 110

Phe Thr Glu Glu Ile Glu Trp Leu Lys Phe Leu Ala Leu Ala Cys Ser  
115 120 125

Ala Leu Gly Val Val Ser  
130

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| TTTTTTTTTT TTTTGTATA GCAATGGAAG AATGGCCTCG TACACACGCT AGAGTGGAAA  | 60   |
| GTCCCAGGCA CCAAGGCTTC CCACCCTAGA AGCAAGCTCA GGGCTTTCTC TTCATCCTTC | 120  |
| CAGGGAGAGC ACTGAGAGAT GATGGGGGGT TGGCAGGGGG CATCCCTTGG ATTATCATTC | 180  |
| TCCAGACTTA GGCTTGAGAG GGAGGGTGGA GAAGTGGATT TCTGGGTCTG GTCCACCTCA | 240  |
| CCTGTTTTCT CAGCTTCTCA CCCACTCAGA GCTCTTGCCC CAATTCTCCC TTTCATCCTG | 300  |
| CAGATCCCTG CGCCTGACTC ATCTCAGGCG AGGAGGCAAA TCATCAGTTA TCTCAGGCAG | 360  |
| CAGCAGGACG AGACTCCTTT CTGATTTTCT CCTTCCCTGG CCACCTCTCC CCACCCCAT  | 420  |
| TTCACTCATT CCAAACCTCT GGCCTCCCCA GCAACTCTAC ATCCTCATCT CCACCTGTTC | 480  |
| CCTCTCTCGA TGCTGTGGGT GACGTTGGAG AGGGAAGCCC GGAGCCCTGA CCTAGTCCGG | 540  |
| CGTGGAGAGA GGAATGGAAA GCAGTGTCCT TTTTGAGAAG GCAAATTTAC AGCTGGCTTT | 600  |
| TGTAATCCTA GCTATTTTTT GTTTGTTTGC TAAGTCTTTG ATAGTCCCCA GTGTGGTTTG | 660  |
| TCTGCCAGTG ATCTCAGCAC CACCAGAGAG CTTGTTAGAA ATGCGGCATC CCAACCCAC  | 720  |
| CACAGCCCTC CCAAGTCAGA TACTGCCACC TCACGAGGCC CCCAGGGAT CCACAAGTTC  | 780  |
| ATTAAAGTTT CAGGAATCCA ATTCTACTAC AAAATATACA TTTATAATTA GGAAAAGGAT | 840  |
| AGTTCTTTTA AATGGTAGAA CTTCCCCAAT GAGTCAGCTA CCTGTATTTT TGGCCTGTCA | 900  |
| GGCTAGACAC TGGAGACCAT TCTGCATAGA ATTGTACCTC CCTGAACTAC TGTTAGGCCT | 960  |
| TAGGGTGGGG ATTCATCTTT CCCTTCTCCC CACCATGGAG ACAAATCCT CTTAAACATA  | 1020 |
| TCCGGGCCTG GCATGGTGGY TMACGCCTCG GCCTCCCAA GTTCTGGGAT TACAGGCATG  | 1080 |

AGCCAYTGTG CCCAGCCACC CGTCACCTGY TAGTGTAGAC AAATGAATAA ACTTAGACAA 1140  
 GCACATGGGC TCCCTCTATA CCAGCCTAGA CTTTGACACT GAAACTCCAT GAGTCTGGGC 1200  
 CACTTCCTGC CACAAGTGTG AATGGAAAAT AAATCATTTT CCAAGGAACC CAAAATCACT 1260  
 AAGCCAAGGA GTCAAGCTGA GAACTTTCAG GCAAACCTGC CCCCCATTTT ATTCCTTAA 1320  
 TAAGAGAGCT ACAAAGATTA AAAAAAAAAA AAAA 1354

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Glu | Ser | Ser | Val | Pro | Phe | Glu | Lys | Ala | Asn | Leu | Gln | Leu | Ala | Phe | 1   | 5   | 10  | 15 |
| Val | Ile | Leu | Ala | Ile | Phe | Cys | Leu | Phe | Ala | Lys | Ser | Leu | Ile | Val | Pro | 20  | 25  | 30  |    |
| Ser | Val | Val | Cys | Leu | Pro | Val | Ile | Ser | Ala | Pro | Pro | Glu | Ser | Leu | Leu | 35  | 40  | 45  |    |
| Glu | Met | Arg | His | Pro | Asn | Pro | Thr | Thr | Ala | Leu | Pro | Ser | Gln | Ile | Leu | 50  | 55  | 60  |    |
| Pro | Pro | His | Glu | Ala | Pro | Gln | Gly | Ser | Thr | Ser | Ser | Leu | Lys | Phe | Gln | 65  | 70  | 75  | 80 |
| Glu | Ser | Asn | Ser | Thr | Lys | Tyr | Thr | Phe | Ile | Ile | Arg | Lys | Arg | Ile | 85  | 90  | 95  |     |    |
| Val | Leu | Leu | Asn | Gly | Arg | Thr | Ser | Pro | Met | Ser | Gln | Leu | Pro | Val | Phe | 100 | 105 | 110 |    |
| Leu | Ala | Cys | Gln | Ala | Arg | His | Trp | Arg | Pro | Phe | Cys | Ile | Glu | Leu | Tyr | 115 | 120 | 125 |    |
| Leu | Pro | Glu | Leu | Leu | Leu | Gly | Leu | Arg | Val | Gly | Ile | His | Leu | Ser | Leu | 130 | 135 | 140 |    |
| Leu | Pro | Thr | Met | Glu | Thr | Lys | Ser | Ser | 145 | 150 |     |     |     |     |     |     |     |     |    |

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

```

CCCCGGTCCC CGCCGCAGCC GCTGCATCCT CCGTGCCCGG CCTGAGCTGG AGTCCCCCGC 60
GCCCCCGCG TTCCGCCCGG CCATGGCTGC GGTGGCGCTG ATGCCACCGC CGCTGCTGCT 120
GCTGCTGCTG TTGGCGTCGC CGCCCGCCGC CTCCGCGCCG TCCGCCCGCG ATCCCTTCGC 180
CCCCCAGCTC GGGGACACGC AGAACTGCCA GCTGCGGTGC CGCGACCGCG ACCTCGGCCC 240
GCAGCCCTCG CAGGCGGGGC TGGAGGGCGC CTCCGAGTCT CCCTATGACA GAGCCGTTCT 300
GATCAGCGCT TGCGAGCGTG GCTGCCGCCT CTTCTCCATC TGCCGATTG TGGCCAGAAG 360
CTCCAAGCCC AATGCCACCC AAAGTGAAGT TGAAGCAGCC TGCGTGGAAG CCTATGTGAA 420
GGAGGCAGAR CAGCAGGCCT GTAGCCACGG CTGCTGGAGC CAGCCCGCGG AGCCTGAGCC 480
GGARCAGAAG AGAAAGGTCC TGGAGGCTCC AAGTGGGGCC CTCTCCCTCT TGGACTTGTT 540
TTCCACCCTC TGCAATGACC TTGTCAACTC AGCCCAGGGA TTTGTCTCCT CCACCTGGAC 600
ATACTACTTG CAGACTGACA ATGGGAAAGT GGTGGTGTTT CAGACTCAGC CCATAGTGGA 660
GAGCCTCGGC TTCCAGGGGG GCCGTCTGCA GCGCGTGGAG GTGACCTGGC GAGGCTCCCA 720
CCCTGAAGCC CTGGAGGTGC ACGTGGACCC TGTAGGCCCC CTGGACAAGG TGAGGAAGGC 780
CAAGATCCGA GTCAAGACCA GCAGCAAGGC CAAGGTGGAG TCTGAAGAGC CACAGGACAA 840
TGAATTCTCT AGTTGCATGT CCCGGCGCTC GGGTCTGCCT CGCTGGATCC TGGCCTGCTG 900
CCTCTTCTCT TCCGTGCTGG TGATGCTGTG GCTGAGCTGC TCCACCCTGG TGACCGCGCC 960
TGGCCAGCAC CTCAAGTTCC AGCCTCTGAC CCTGGAGCAG CACAAGGGCT TCATGATGGA 1020
GCCCCATTGG CCCCTGTACC CGCCGCCGTC CCACGCCTGT GAGGACAGCC TACCACCCTA 1080
CAAGCTGAAG CTGGACCTGA CCAAGCTGTA GGCCTCCACT GGCCCCATCA CTGCCAACTG 1140
CAGGGGGCCC CTCGGGCCTC ACTTGCCCTG AGCCCAGGAG TCCAAGGGCA GGGTGGGTCC 1200
AGCGTTGAGC CCCTCCACCC CCAAATCCTT CCTCTCCTCC CAGTCCCACC CCTTGCCCCA 1260
CGGAGTCCTG GGGACGCAGT GCCCCAGCTG GGAAGAGGGC GGGATCGGGC ACTGGTTCCT 1320
CCTTGTCCTC GCTTTCTTGG GGGCTTGCTA CTTTTTGTCT TCTATTGTGT GGCTTTCTGA 1380
GTATTTGAAC CCCAGTCCTG TGTCACCTTC CTTTTTCCTT CTATGTCCCC TCTCTGCGGG 1440
GGGGGCGCTG AGGCTGAGGG GGAGCTGCGT CTTGCTAGGG CTTCCCCCTT CTCCCCATCC 1500
CGGTCTCCAG AGACCCAGCT TCTGAGAGAC AGGGTGTGGG CATCTCCATG CCCCTATAAA 1560
GCGTGCCTGG GGCTTGCTCT GGGCTGGGGA GGAATAAACC ATGTATATAA AAGAAAAAAA 1620
AAAAAAA 1628

```

(2) INFORMATION FOR SEQ ID NO:218:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Ala | Ala | Val | Ala | Leu | Met | Pro | Pro | Pro | Leu | Leu | Leu | Leu | Leu | Leu | 1   | 5   | 10  | 15 |
| Leu | Ala | Ser | Pro | Pro | Ala | Ala | Ser | Ala | Pro | Ser | Ala | Arg | Asp | Pro | Phe | 20  | 25  | 30  |    |
| Ala | Pro | Gln | Leu | Gly | Asp | Thr | Gln | Asn | Cys | Gln | Leu | Arg | Cys | Arg | Asp | 35  | 40  | 45  |    |
| Arg | Asp | Leu | Gly | Pro | Gln | Pro | Ser | Gln | Ala | Gly | Leu | Glu | Gly | Ala | Ser | 50  | 55  | 60  |    |
| Glu | Ser | Pro | Tyr | Asp | Arg | Ala | Val | Leu | Ile | Ser | Ala | Cys | Glu | Arg | Gly | 65  | 70  | 75  |    |
| Cys | Arg | Leu | Phe | Ser | Ile | Cys | Arg | Phe | Val | Ala | Arg | Ser | Ser | Lys | Pro | 85  | 90  | 95  |    |
| Asn | Ala | Thr | Gln | Thr | Glu | Cys | Glu | Ala | Ala | Cys | Val | Glu | Ala | Tyr | Val | 100 | 105 | 110 |    |
| Lys | Glu | Ala | Glu | Gln | Gln | Ala | Cys | Ser | His | Gly | Cys | Trp | Ser | Gln | Pro | 115 | 120 | 125 |    |
| Ala | Glu | Pro | Glu | Pro | Glu | Gln | Lys | Arg | Lys | Val | Leu | Glu | Ala | Pro | Ser | 130 | 135 | 140 |    |
| Gly | Ala | Leu | Ser | Leu | Leu | Asp | Leu | Phe | Ser | Thr | Leu | Cys | Asn | Asp | Leu | 145 | 150 | 155 |    |
| Val | Asn | Ser | Ala | Gln | Gly | Phe | Val | Ser | Ser | Thr | Trp | Thr | Tyr | Tyr | Leu | 165 | 170 | 175 |    |
| Gln | Thr | Asp | Asn | Gly | Lys | Val | Val | Val | Phe | Gln | Thr | Gln | Pro | Ile | Val | 180 | 185 | 190 |    |
| Glu | Ser | Leu | Gly | Phe | Gln | Gly | Gly | Arg | Leu | Gln | Arg | Val | Glu | Val | Thr | 195 | 200 | 205 |    |
| Trp | Arg | Gly | Ser | His | Pro | Glu | Ala | Leu | Glu | Val | His | Val | Asp | Pro | Val | 210 | 215 | 220 |    |
| Gly | Pro | Leu | Asp | Lys | Val | Arg | Lys | Ala | Lys | Ile | Arg | Val | Lys | Thr | Ser | 225 | 230 | 235 |    |
| Ser | Lys | Ala | Lys | Val | Glu | Ser | Glu | Glu | Pro | Gln | Asp | Asn | Asp | Phe | Leu | 245 | 250 | 255 |    |
| Ser | Cys | Met | Ser | Arg | Arg | Ser | Gly | Leu | Pro | Arg | Trp | Ile | Leu | Ala | Cys | 260 | 265 | 270 |    |

Cys Leu Phe Leu Ser Val Leu Val Met Leu Trp Leu Ser Cys Ser Thr  
 275 280 285

Leu Val Thr Ala Pro Gly Gln His Leu Lys Phe Gln Pro Leu Thr Leu  
 290 295 300

Glu Gln His Lys Gly Phe Met Met Glu Pro Asp Trp Pro Leu Tyr Pro  
 305 310 315 320

Pro Pro Ser His Ala Cys Glu Asp Ser Leu Pro Pro Tyr Lys Leu Lys  
 325 330 335

Leu Asp Leu Thr Lys Leu  
 340

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TCGGGCGGCG GAGTAGCAAG TGGCCATGGG GAGCCTCAGC GGTCTGCGCC TGGCAGCAGG | 60  |
| AAGCTGTTTT AGGTTATGTG AAAGAGATGT TTCCTCATCT CTAAGGCTTA CCAGAAGCTC | 120 |
| TGATTTGAAG AGAATAAATG GATTTTGCAC AAAACCACAG GAAAGTCCCG GAGCTCCATC | 180 |
| CCGCACTTAC AACAGAGTGC CTTTACACAA ACCTACGGAT TGGCAGAAAA AGATCCTCAT | 240 |
| ATGGTCAGGT CGTTCAAAA AGGAAGATGA AATCCCAGAG ACTGTCTCGT TGGAGATGCT  | 300 |
| TGATGCTGCA AAGAACAAGA TGCGAGTGAA GATCAGCTAT CTAATGATTG CCCTGACGGT | 360 |
| GGTAGGATGC ATCTTCATGG TTATTGAGGG CAAGAAGGCT GCCCAAAGAC ACGAGACTTT | 420 |
| AACAAGCTTG AACTTAGAAA AGAAAGCTCG TCTGAAAGAG GAAGCAGCTA TGAAGGCCAA | 480 |
| AACAGAGTAG CAGAGGTATC CGTGTTGGCT GGATTTTGAA AATCCAGGAA TTATGTTATA | 540 |
| ACGTGCCTGT ATTAAAAAGG ATGTGGTATG AGGATCCATT TCATAAAGTA TGATTTGCCC | 600 |
| AAACCTGTAC CATTTCCGTA TTTCTGCTGT AGAAGTAGAA ATAAATTTTC TTAAATAAAA | 660 |
| AAAAAAAAA A                                                       | 671 |

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Ser | Leu | Ser | Gly | Leu | Arg | Leu | Ala | Ala | Gly | Ser | Cys | Phe | Arg |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Cys | Glu | Arg | Asp | Val | Ser | Ser | Ser | Leu | Arg | Leu | Thr | Arg | Ser | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asp | Leu | Lys | Arg | Ile | Asn | Gly | Phe | Cys | Thr | Lys | Pro | Gln | Glu | Ser | Pro |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gly | Ala | Pro | Ser | Arg | Thr | Tyr | Asn | Arg | Val | Pro | Leu | His | Lys | Pro | Thr |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asp | Trp | Gln | Lys | Lys | Ile | Leu | Ile | Trp | Ser | Gly | Arg | Phe | Lys | Lys | Glu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Asp | Glu | Ile | Pro | Glu | Thr | Val | Ser | Leu | Glu | Met | Leu | Asp | Ala | Ala | Lys |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asn | Lys | Met | Arg | Val | Lys | Ile | Ser | Tyr | Leu | Met | Ile | Ala | Leu | Thr | Val |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val | Gly | Cys | Ile | Phe | Met | Val | Ile | Glu | Gly | Lys | Lys | Ala | Ala | Gln | Arg |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| His | Glu | Thr | Leu | Thr | Ser | Leu | Asn | Leu | Glu | Lys | Lys | Ala | Arg | Leu | Lys |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Glu | Glu | Ala | Ala | Met | Lys | Ala | Lys | Thr | Glu |     |     |     |     |     |     |  |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CACAAGAGGA GTTACTTGTT CCAGCCTCCT GTGTGGACTG CTTTCCTATC AAAGCACCTT | 60  |
| AGACATGCAC GAGGAAGAAA TATACACCTC TCTTCAGTGG GATAGCCCAG CACCAGACAC | 120 |
| TTACCAGAAA TGTCTGTCTT CCAACAAATG TTCAGGAGCA TGCTGTCTTG TGATGGTGAT | 180 |
| TTCATGTGTT TTCTGCATGG GATTATTAAC GGCATCCATT TTCTTGGGCG TCAAGTTGTT | 240 |
| GCAGGTGTCC ACCATTGCGA TGCAGCAGCA AGAAAACTC ATCCAACAAG AGAGGGCACT  | 300 |
| GCTAAACTTT ACAGAATGGA AGAGAAGCTG TGCCCTTCAG ATGAAATATT GCCAAGCCTT | 360 |
| CATGCAAAAC TCATTAAGTT CAGGATTTTA TCACTGGCAG CTTGAGGAAG ATTAAGGAA  | 420 |
| GCTATGATTA CTGGGTGGGG TTGTCTCAGG ATGGACACAG CGGACGCTGG CTTTGGCAAG | 480 |
| ATGGCTCCTC TCCTTCTCCT GGCCTGTTGC CAGCAGAGAG ATCCCAGTCA GCTAACCAAG | 540 |

TCTGTGGATA CGTGAAAAGC AATTCCCTTC TTTCGTCTAA CTGCAGCACG TGGAAGTATT 600  
 TTATCTGTGA GAAGTATGCG TTGAGATCCT CTGTCTGAAA GAAATTGTGT TCAAAGTGTT 660  
 CTATTACACT GTTATTTTGA GCATGCCATT GGAAAACCCA CCCCCACCCC CCCTCAAAAA 720  
 AACAGAACAG TAAACCAAAA TGTGGGCCAT GAAATTAGCA ACCTGGGACT CAATAATACA 780  
 CTTGGGAATA TTCTTCACA CCGTCCAGAT TTCATTTGAT GTTGTTTACA TTGCAAGAGT 840  
 AAAACTTATT TAGAGCTACA GAAGACAAAA CCCTGAAGAG TTAAGAACAA ACGCAAGGAA 900  
 ATAATTTTTA TTGTTTAAAG CCCGGAATGA CTGTAACTTT CACACAAGGT ACGCATCTAT 960  
 GTTTTTGGGG GAGGTGATGT AGTTACAGCT GACTAATATT TTTAAAATAA ATAAATAAAT 1020  
 TTGGCCTTTA AAACCTCAAAA AAAAAAAAAA AAAAAA 1056

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Met His Glu Glu Glu Ile Tyr Thr Ser Leu Gln Trp Asp Ser Pro Ala  
 1 5 10 15  
 Pro Asp Thr Tyr Gln Lys Cys Leu Ser Ser Asn Lys Cys Ser Gly Ala  
 20 25 30  
 Cys Cys Leu Val Met Val Ile Ser Cys Val Phe Cys Met Gly Leu Leu  
 35 40 45  
 Thr Ala Ser Ile Phe Leu Gly Val Lys Leu Leu Gln Val Ser Thr Ile  
 50 55 60  
 Ala Met Gln Gln Gln Glu Lys Leu Ile Gln Gln Glu Arg Ala Leu Leu  
 65 70 75 80  
 Asn Phe Thr Glu Trp Lys Arg Ser Cys Ala Leu Gln Met Lys Tyr Cys  
 85 90 95  
 Gln Ala Phe Met Gln Asn Ser Leu Ser Ser Gly Phe Tyr His Trp Gln  
 100 105 110  
 Leu Glu Glu Asp  
 115

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

ANATTAGATC TGTTTCCATT TCCCAGGCA

29

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TNGCGTGAGA TCAACTACTC TGCCTGTGA

29

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

ANACAGGACC GAGTCGAGAA GCCAAAGAC

29

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

ANGGGACAAT GCAAACGCAA GAGCTGGGC

29

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

ANGAGGCATG TTTATCATCA GCCCTGCAG

29

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

ANATTTGCCT TCTCAAAGG GACACTGCT

29

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GNTGGGACTG GGAGGAGAGG AAGGATTTG

29

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GNAACGCCAT AAGCATGTCC TTCTAATGT

29

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

ATTY DOCKET NO.: GIN-6054CP

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

CNTGAAATCA CCATCACAAG ACAGCATGC

29

ATTYDOCKETNO:GIN-6054CP

1

105